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US-10-425-115-13680 US-10-425-115-13680 US-10-425-115-13670 US-10-425-115-13670 US-10-425-115-136713 US-10-425-115-136713 US-10-425-115-145027 US-10-425-115-14544 US-10-425-115-44746 US-10-425-115-44746 US-10-425-115-44748 US-10-425-115-44775 US-10-425-115-44775 US-10-425-115-44775 US-10-425-115-44775

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APPLICANT: Dubois, Patrice
APPLICANT: Malven, Marianne
APPLICANT: Malven
TITLE OF INVENTION: OF GENE EXPRESSION
FILE REFERENCE: 38-21(15678) B promoters
CURRENT APPLICATION NUMBER: US/09/846,903
CURRENT APPLICATION NUMBER: US 60/201,255
PRIOR PRILNG DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 90
LENGTH: 823
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Publication No. US20030200565A1
GENERAL INFORMATION:
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; ORGANISM: Zea mays
US-09-846-903-90
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Sequence 18768, A
Sequence 31817, A
Sequence 69837, A
GENERAL INFORMA
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Sequence 34629, A
Sequence 57384, A
Sequence 145839,
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74208, A
36797, A
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60268, A
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Sequence 16, Appl
                                                                                                                                                       March 5, 2006, 10:17:20 ; Search time 824 Seconds (without alignments) 8259.342 Million cell updates/sec
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1: /cgn2 6/ptodata/1/pubpna/USO7 PUBCOMB.seq:*
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4: /cgn2_6/ptodata/1/pubpna/USO8 PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/USO8 PUBCOMB.seq:*
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Copyright (c) 1993 - 2006 Blocceleration Ltd.
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APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwel
APPLICANT: Cao, Yongwel
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
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US-10-425-114-22826
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Pred: No. 5.2e-59;
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Publication No. US200440034888A1
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Best Local Similarity 92.4%;
Matches 243; Conservative
    Conservative
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FEATURE:
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APPLICANT: Conner, Timothy W.
APPLICANT: Dubois, Parrice
APPLICANT: Dubois, Parrice
APPLICANT: Malven, Marianne
APPLICANT: Masucci, James D.
ATTLE OF INVENTION: PLANT REGULATORY SEQUENCES FOR SELECTIVE CONTROL
TITLE OF INVENTION: OF GENE EXPRESSION
TITLE REFERENCE: 38-21 (15678) B promoters
CURRENT APPLICATION NUMBER: US/10/660,208
PRIOR APPLICATION NUMBER: US 60/201,255
PRIOR APPLICATION NUMBER: US 60/201,255
NUMBER OF SEQ ID NOS: 98
                                             Length 1587;
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                                        Score 564; DB Pred. No. 1.8e. 0; Mismatches
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Publication No. US20040133946A1
GENERAL INFORMATION:
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llarity 99.1%;
Conservative
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Best Local Similarity
Matches 567; Conserv
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Best Local Similarity
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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement; FILE REPERENCE: 38-21 (53313) B CURRENT APPLICATION NUMBER: US/10/425,114 CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 73128 SEQ ID NO 31817
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US-10-425-114-31817
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Best Local Similarity 91.1%;
Matches 245; Conservative
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ORGANISM: Zea maye
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ORGANISM: Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Salou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 18768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     271 haaaanatengrenakeananteantengreeaaneaageanteaanaantaaagea 330
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                                                                                                                                                                                              874 ATATOTTGAGTTTTTTTTACATTCACCCCCTAAACACACTCGAAGACATAACTCAAGACA 815
1054 TGCACGGTACTCCCAAGTATAAGACACACTAAAACACACAAAATACAGTGGACGTGTCT 995
                                                                    AAAACATGTGTCTTACCATATTCATTGTATCAGAACATTCAATAAATTAAAGTGAC 121
                                                                                                                994 AAAACATGTGTCTTACCATATTAATTGTACCAATCAGAGCATTCAATAAATTAAAGTGAC 935
                                                                                                                                                              CAATCAGATAGTCTCCTGTCCCGAATATAGAGCTAAGACACTGTGTGTTCTTCGTCAAGATAC 181
                                                                                                                                                                                                                                                           182 ATGTCTTGAGATTTTTTACATTCACCCCCTAGACACACTCTAAGACACACTTAAGACA 241
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92.3%; Pred. No. 1.3e-58;
ive 0; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , OTHER INFORMATION: Clone ID: MRT4577_117117C.1
US-10-425-115-18768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 18768, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        242 CCCATTGTACATGCCCTAACTGG 264
                                                                                                                                                                                                                                                                                                                                                                                                 814 cccacreracareceraares 792
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Best Local Similarity 92.3
Matches 241; Conservative
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ORGANISM: Zea mays
                                                                                                                                                                 122
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Length 1326;

Score 220.2; DB 7; Length 1 Pred. No. 9.1e-56; 0; Mismatches 23; Indels

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GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Notleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plante
FILE REFERENCE: 38-21(5322) B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NOS: 369326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CTGCACGGTACTCCAAGTATAAGACACAGCTAAAACACAACATAATGCAGTGGTCATGTC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 220.2; DB 8;
Pred. No. 1.4e-55;
0; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: MRT4577_163683C.1 US-10-425-115-69837
Sequence 69837, Application US/10425115
Publication No. US20040214272A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26.8%;
91.1%;
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Best Local Similarity 91.1:
Matches 245; Conservative
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Sequence 31817, Application US/10425114 Publication No. US20040034888A1

GENERAL INFORMATION

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1475 GACCAATCAGCTAGCCTCCTGTCTCGAACATAGAGCTAAGACATTGTGTCTTCGTCAAGA 1534
                                                                                                 1535 TACATGICTITAGGITTITITATATTCACTCCCAAGACACACTCTAAGACACAACGTAAC 1594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Woosley, Aaron
TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants
NUMBER OF SEQUENCES: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 9299;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                    179 TACATGTCTTGAGATTTTTTACATTCACCCCCCTAGACACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.18-52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/10/759,602
FILING DATE: 16-Jan-2004
CLASSIPICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 209.2;
Pred. No. 6.1
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MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-759-602-15
                                                                                                                                                                                                                                                                                                                                                  Publication No. ....
GENERAL INFORMATION:
Antley, Michael
APPLICANT: Ainley, Michael
Belmar, Scott
Folkerts, Otto
Hopkins, Nicole
Menke, Michael A.
Pareddy, Dayakar
Petcolino, Joseph F.
Smith, Kelley
Smith, Relley
                                                                                                                                                                                                    1595 ACACCCATTGTACATGCTCTTA 1616
                                                                                                                                                     239 ACACCCATTGTACATGCCCTAA 260
                                                                                                                                                                                                                                                                                                                               Sequence 15, Application US/10759602
Publication No. US20040143868A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Kraus, Eric'J
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Indianapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match . 25.4
Best Local Similarity 90.1
Matches 236; Conservative
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2458 CCTATCAGCTAGTCTCCTGTCTCCAACATAGAGCTAAGACATTGTGTCTTCGTCAAGATA 2399
                                                                                                                           2518 TAAAACATGTGTGTTTACCATATTCATCTACCAATCAGAGCATTCAATAAATTAAAGTGA 2459
                                                                                                                                                                                                                                                                                                                               2398 CATGTCTTGAGTTTTTTTACATTCA-CCCCTTAGACACTTTAAGACACAACTTAAGAC 2340
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                                                                              CATTGTATCAATCAGAACATTCAATAAATTAAAGTGA 120
                                                                                                                                                                             CCAATCAGATAGTCTCCTGTCCCGAATATAGAGCTAAGACACTGTGTGTCTTCGTCAAGATA 180
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TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 7; Length 6550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                   2339 ACATATTGTACATGCCCTAAGGGGAGTCG 2311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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APPLICATION NUMBER: US/10/759,602
FILING DATE: 16-Jan-2004
CLASSIFICATION: «UMKNOWN»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-759-602-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 9330 Zionsville Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Menke, Michael A.
Pareddy, Dayakar
Petolino, Joseph F.
Smith, Kelley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Folkerts, Otto
Hopkins, Nicole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ainley, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 90.1
Matches 236; Conservative
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                            2578
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SERVING INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Abua
APPLICANT: Shou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Gao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: NUMBER: US/10/425,114
CURRENT APPLICATION NUMBER: 10910/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
                                                                                                                                                                                                                                                                                                        Publication No. US2040214272A1

Publication No. US2040214272A1

GRNERAL INFORMATION:

GRNERAL INFORMATION:

GRNERAL INFORMATION:

APPLICANT: La Royalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Thou, Yihua

APPLICANT: Con INVENTION: Plants

TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

SEQ ID NO 134827

LENGTH: 814
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1528 GACCAATCAGCTAGCCTCCTGTCTCGAACATAGAGCTAAGACATTGTGTCTTCGTCAAGA 1587
                                                                                               CTAAGACACAACGTAAC 1647
                                                 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             814 IGICIAAACAIGICITAICAIATICAITGIACCAAICAAAACAIICAAIAAAITAAAGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 179.6; DB 8; Length Pred. No. 1.6e-43; O; Mismatches 14; Indels
                                                                                  , OTHER INFORMATION: Clone ID: MRT4577_54445C.1
US-10-425-115-134827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 23949, Application US/10425114 Publication No. US20040034888A1
                                                                                                                                                                                                 1648 ACACCCATIGTACATGCTCTTA 1669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     239 ACACCCATTGTACATGCCCTAA 260
                                                                                                                                                   239 ACACCCATTGTACATGCCCTAA 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 93.1%;
Matches 188; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                   US-10-425-115-134827/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -10-425-114-23949/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1468 TCTAAAACATGTGTCTTACCATATTCATTGTACCAATTAGAACATTTAATAAATTAAGT 1527
          1522 GACCAATCAGCTAGCCTCCTGTCTCGAACATAGAGCTAAGACATTGTGTCTTCGTCAAGA 1581
                                                                                                       1582 TACATGTCTTAAGTTTTTTTTTTTTTCACTCCCAAGACACACTCTAAGACACACAAGACAAGAAG 1641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 TCTAAAACATGTGTCTTACCATATTCATTGTATCAATCAGAACATTCAATAAATTAAAGT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 GACCAATCAGATAGTCTCCTGTCCCGAATATAGAGCTAAGACACTGTGTCTTCGTCAAGA 178
                                                           179 TACATGTCTTGAGATTTTTTACATTCACCCCCTAGACACACTCTAAGACACAACTTAAG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 TGCACGGTACTCCAAGTATAAGACACAGCTAAAACACATAATG---CAGTGGTCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Moosley, Aaron
TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants
NUMBER OF SECUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>ښ</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/759,602
FILING DATE: 16-Jan-2004
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 25.4%; Score 209.2; DB 7; Best Local Similarity 90.1%; Pred. No. 6.1e-52; Matches 236; Conservative 0; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: circular

MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 16:.
US-10-759-602-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: DowAgroSciences LI
STREET: 9330 Zionsville Road
                                                                                                                                                                                                                                                                                                                                                                                                                               Armstrong, Katherine
Belmar, Scott
Folkerts, Otto
Hopkins, Nicole
                                                                                                                                                                                         1642 ACACCCATTGTACATGCTCTTA 1663
                                                                                                                                                          ACACCCATTGTACATGCCCTAA 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Kraus, Eric J
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                          Sequence 16, Application US/10759602
Publication No. US20040143868A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Menke, Michael A.
Pareddy, Dayakar
Perolino, Joseph F
Smith, Kelley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 317 337 51.
TELEFAX: 317 337 4847
INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ainley, Michael
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Indiana
COUNTRY: USA
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TYPE: DNA
ORGANISM: Zea mays
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                                                                                                                                                                                                                                                                                                                                   361 GTCTTGAGATTTTTTACATTCACCCCCTAGACACACTCTAAGACACACTTAAGACACC 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              379 caraacraaaacacaacaraararaaragrcargrcraaaacarargrcrrarcararrc 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     259 AACATAGAGCTAAGACACTGTGTCTTCGTCAAGATACATGTCTTGAGTCTTTTAACATTT 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         205 ACCCCCTAGACACACTCTAAGACACATTAAGACACCCCATTGTACATGCCCTAACTGG 264
                                                                                                                                                                                                                                            ATCAGATAGTCTCCTGTCCCGAATATAGAGCTAAGACACTGTGTGTCTTCGTCAAGATACAT 183
                                                                                                                                                                                                                                                                                                               GTCTTGAGATTTTTTACATTCACCCCCTAGACACACTCTAAGACACAACTTAAGACACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85 ATTGTATCAATCAGAACATTCAATAAATTAAAGTGACCAATCAGATAGTCTCCTGTCCCG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     145 AATATAGAGCTAAGACACTGTGTCTTCGTCAAGATACATGTCTTGAGATTTTTTACATTC 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 CACAGCTAAAACACATAATGCAGTGGTCATGTCTAAAACATGTGTCTTACCATATTC 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 AACATGTGTCTTACCATATTCATTGTATCAGAACATTCAATAAATTAAAGTGACCA
                                                                                                                                        0; Gaps
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21.6%; Score 177.8; DB 8; Length 379;
Best Local Similarity 86.3%; Pred. No. 3.8e-43;
Matches 208; Conservative 0; Mismatches 32; Indels 1
                                                                                                        Length 485;
                                                                                                  Score 179.4; DB 7; Length
Pred. No. 1.4e-43;
0; Mismatches 11; Indels
                                  ; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3606-031-G10_FLI
US-10-425-114-23949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , OTHER INFORMATION: Clone ID: MRT4577_131586C.1 US-10-425-115-34629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (1)..(379)
OTHER INFORMATION: unsure at all n locations
FEATURE:
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Publication No. US20040214272A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                     244 CATTGTACATGCCCTAA 260
                                                                                                                                                                                                                                                                                                                                                                                                         CACTGTACATGCCCTTA 285
                                                                                                    Query Match
21.8%;
Best Local Similarity 94.4%;
Matches 186; Conservative (
TYPE: DNA
ORGANISM: Zea mays
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Scoul, Vibua
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
TITLE OF INVENTION: NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NOS: 369326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 CANTCAGATAGTCTCCTGTCCCGAATATAGAGCTAAGACACTGTGTCTTCGTCAAGATAC 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182 ATGTCTTGAGATTTTTACATTCACCCCCTAGACACACTCTAAGACACATTAAGACA 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 AAACATGGGGGCTTACCATATTCATTTACCAATCAGAGCTTTCAATAAATTAAAGGGAC 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 AAAACATGTGTCTTACCATATTCATTGTATCAATCAGAACATTCAATAAATTAAAGTGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 143.2; DB 8;
Pred. No. 1.4e-32;
0; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Clone ID: MRT4577_152328C.1
US-10-425-115-57384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187 cccacrerareccereacaaeeccaaaac 218
                                                                                                                                                                                                                                                                    Sequence 57384, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
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Job time : 825 secs
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Best Local Similarity 79.7%;
Matches 169; Conservative
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159940 rgráragrárgrigrírfrárakárakárakákákákákákákákákákákáká 159881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               292 CCAACCATGTACAGTTGTTGCAACGTGAATGGTTATTTGCTTCAGATTAAAGCTAATTAT 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    159880 CACACACACACACACACTTCTATTGGAATTATGATGGCTACCTTCAGCCTGAAAGGAAA
                                                                     00000000000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
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Sequence 652867,
Sequence 64389, A
Sequence 64389, A
Sequence 9452, Ap
Sequence 3542, Ap
Sequence 3542, Ap
Sequence 368, App
Sequence 368, App
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Sequence 308, App
Sequence 671953,
                                                                                                                     March 5, 2006, 11:08:25; Search time 513 Seconds (without alignments) 3517.379 Million cell updates/sec
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Sequence 34470,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                            US-10-660-208-90
823
1 ctgcacggtactccaagtat......cgatccattctccagcgcag 823
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Published Applications NA New:*

1: /cgn2_6/prodata/1/pubpna/USOB NEW PUB.seq:*
2: /cgn2_6/prodata/1/pubpna/USOB_NEW_PUB.seq:*
3: /cgn2_6/prodata/1/pubpna/USOB_NEW_PUB.seq:*
4: /cgn2_6/prodata/1/pubpna/USOB_NEW_PUB.seq:*
5: /cgn2_6/prodata/1/pubpna/USOB_NEW_PUB.seq:*
6: /cgn2_6/prodata/1/pubpna/USOB_NEW_PUB.seq:*
7: /cgn2_6/prodata/1/pubpna/USOB_NEW_PUB.seq:*
8: /cgn2_6/prodata/1/pubpna/USOB_NEW_PUB.seq:*
9: /cgn2_6/prodata/1/pubpna/USOB_NEW_PUB.seq:*
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11: /cgn2_6/prodata/1/pubpna/USOB_NEW_PUB.seq:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-09-925-065A-715739

US-09-925-065A-715739

US-09-925-065A-717296

US-09-925-065A-652867

US-10-750-185-64389

US-10-750-185-64389

US-10-750-185-64389

US-10-925-065A-63919

US-09-925-065A-192068

US-09-925-065A-192068

US-09-925-065A-192068

US-09-925-065A-487030

US-09-925-065A-487030

US-10-330-773-308

US-09-925-065A-487030

US-10-330-773-308

US-10-925-065A-487030

US-10-925-065A-487030
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Maximum Match 100%
Listing first 45 summaries
                                                                                        nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Perfect score:
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Publication No. US20060040262A1
| GENERAL INFORMATION:
| APPLICANT: David W. Morris
| APPLICANT: David W. Morris
| APPLICANT: David W. Morris
| APPLICANT: David W. Wortis
| CURRENT APPLICATION NOWEL 102/10/330,773
| CURRENT FILING DATE: 2002-12-27
| NUMBER OF SEQ ID NOS: 981
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 23
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US-10-330-773-710
US-09-925-065A-140955
US-09-925-065A-131391
US-09-925-065A-331391
US-09-925-065A-447145
US-09-925-065A-447145
US-09-925-065A-4400
US-09-925-065A-784400
US-09-925-065A-781578
US-09-925-065A-781578
US-09-925-065A-781578
US-09-925-065A-781578
US-09-925-065A-78178
US-09-925-065A-78178
US-09-925-065A-781775
US-09-925-065A-781775
US-09-925-065A-781775
US-09-925-065A-781775
US-09-925-065A-781775
US-09-925-065A-781775
US-09-925-065A-781775
US-09-925-065A-781775
US-09-925-065A-781775
US-10-750-623-49985
US-10-750-623-4144
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Query Match
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                                                                                                                                                                                                                                                                      Sequence 715777, Application US/09925065A

Sequence 715777, Application US/09925065A

Publication No. US20040181048A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single

TITLE OF INVENTION: Identification and Mapping of Single

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A

PRIOR PELING DATE: 2000-10-8-08

PRIOR PELING DATE: 2000-10-24

PRIOR PELING DATE: 2000-11-30

PRIOR PELING DATE: 2000-11-30

PRIOR PELING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/250,766

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR APPLICATION NUMBER: US 60/260,766

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR APPLICATION NUMBER: US 60/260,766

PRIOR APPLICATION NUMBER: US 60/260,766
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR PILING DATE: 2000-10-24
PRIOR PILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2000-11-30
PRIOR PLING DATE: 2000-11-30
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Pred. No. 4.
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Publication No. US20040181048A1
GENERAL INFORMATION:

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Best Local Similarity 51.5<sup>3</sup>
Matches 86, Conservative
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CORGANISM: Homo sapiens
US-09-925-065A-715737
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4.5%; Score 37.4; Di
Best Local Similarity 51.5%; Pred. No. 4.8;
Matches 86; Conservative 0; Mismatches
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RRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SEQ ID NOS: 957086
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PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBERS: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 715738
LENGTH: 2010
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Local Similarity 51.5%;
les 86; Conservative 0
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CORGANISM: Homo sapiens
US-09-925-065A-715738
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US-09-925-065A-652867
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US-10-750-623-64389
                                                  TYPE: DNA ORGANISM:
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR PLING DATE: 2000-11-20
PRIOR PLING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: US 60/250,092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match

4.4%; Score 36.4; DB 6; Length 1148;
Best Local Similarity 45.9%; Pred. No. 7.2;
Matches 124; Conservative 0; Mismatches 146; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches 146;
APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of
TITLE OF INVENTION: Nucleotide Polymorphisms in t.
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-11-24
PRIOR PILING DATE: 2000-11-20
PRIOR PLING DATE: 2000-11-20
PRIOR PLING DATE: 2000-11-30
PRIOR PLING DATE: 2000-11-30
PRIOR PLING DATE: 2001-01-6
PRIOR PLING DATE: 2001-01-6
PRIOR PILING DATE: 2001-01-6
PRIOR PILITATION NUMBER: US 60/261,766
PRIOR PILING DATE: 2001-01-6
PRIOR PILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FRAESEQ for Windows Version 4.0
LENGTH: 1148
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Publication No. US20040181048A1
GENERAL INFORMATION:
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US-09-925-065A-71729
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942 AACTGTATTAAACTGTTGAAAGTTTTTAATTTTCATTACTTTAAATGGGAATTATGAACTT 1001
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APPLICANT: MMI GENOMICS, INC.

APPLICANT: DENISE, Sue K.

APPLICANT: DENISE, Sue K.

APPLICANT: MCICANTE, DENISE, Stephen

APPLICANT: HOSENFELD, David

APPLICANT: HOSENFELD, Dennis

TITLE OF INVESTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

FILE REFERENCE: MMIL100-2.31

CURRENT APPLICATION NUMBER: US/10/750, 185

CURRENT APPLICATION NUMBER: US 60/437, 482

PRIOR APPLICATION NUMBER: US 60/437, 482

PRIOR APPLICATION NUMBER: US 60/437, 482

SOFTWARE: PALENTIN VERSION 3.1

SEQ ID NO 64389

LENGTH: 1829
                                                                                                                                                                                                                                                                                                                                       Score 36; DB-6; Length 415;
Pred. No. 6;
1; Mismatches 71; Indels
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Pred. No. 11;
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PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FASTSEQ for Windows Version 4.0
'SEQ ID NO 652867
LENGTH: 41S
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Publication No. US20050260603A1
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) ORGANISM: Bovine 19866880119920
US-10-750-185-64389
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Best Local Similarity 52.0%;
Matches 78; Conservative
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Best Local Similarity 50.0%;
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LENGTH: 1457619
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TITLE OF INVENTION: NUCLEIC ACID AND POLYBEPTIDE SEQUENCES
TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
FILE REPERENCE: 09531-128001
CURRENT APPLICATION NUMBER: US/11/098,686
CURRENT FILING DATE: 2005-04-04
PRIOR FILING DATE: 2003-10-01
PRIOR FILING DATE: 2003-10-01
PRIOR FILING DATE: 2003-10-04
PRIOR FILING DATE: 2002-10-04
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                                                                                                                                             APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REPRESENCE: MAIL100-1
CURRENT APPLICATION NABER: US/10/750,623
CURRENT FILING DATE: 2003-12-31
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4.4%; Score 36; DB 12; Length 4149;
Best Local Similarity 45.0%; Pred. No. 16;
Matches 135; Conservative 0; Mismatches 165; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 36; DB 8; Length 1829;
Pred. No. 11;
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50.0%; Pred. No. 11,
... 0; Mismatches
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SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PALENTIN VETSION 3.1
SEQ ID NO 64389
Application US/10750623
US20050287531A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9452, Application US/11098686
Publication No. US20060024696A1
GENERAL INFORMATION:
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US-11-098-686-9452
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US-10-750-623-64389
                                                            APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 50.03
Matches 90; Conservative
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LENGTH: 4149
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680457 acaaderidaaceridaraacaacreridaaridekarraarakericareaaaakaaaradarake 680516
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Publication No. US20060024696A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: PROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
TITLE OF INVENTION: PROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
TITLE OF INVENTION: PROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
TITLE OF INVENTION: PROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
CURRENT APPLICATION NUMBER: US/11/098,686
CURRENT FILING DATE: 2005-04-04
PRIOR PRILING DATE: 2003-10-01
PRIOR FILING DATE: 2003-10-01
PRIOR FILING DATE: 2002-10-04
NUMBER OF SQ ID NOS: 11433
SOFTWARE: FRASECEQ for Windows Version 4.0
SEQ ID NO 8739
3162 ACACATTGAACCTATAGTAACAACAAATGATATACATAAAAATAACCTATTAGAGAATGG 3221
                                                                                                                                                                                     3222 TACATCTTTTAATGAAAATCAGTTATACTACAAAACTCTATAGAGATACCTGAAGATTT 3281
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                                                                                                                    136 CCTGTCCCGAATATAGAGCTAAGACACTGTGTCTTCGTCAAGATACATGTCTTGAGATTT
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4.4%; Score 36; DB 12; Length 14
Best Local Similarity 45.0%; Pred. No. 1.8e+02;
Matches 135; Conservative 0; Mismatches 165; Indels
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; ORGANISM: Lawsonia intracellularis
US-11-098-686-8739
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         282 IATTCAAGAACCAACCATGTACAGTTGTTGCAACGTGAATGGTTATTTGCTTCAGATTAA 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       311 TATTCAAATGAGCACAAAACAATATTTATTCAGAGCTGCCTATATTCAGAGCTGGCTAT 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Novel Compositions and Methods in Cancer FILE REFERENCE: 529452001300
CURRENT APPLICATION VMBER: 108/10/330,773
CURRENT PILING DATE: 2002-12-27
NUMBER OF SEQ ID NOS: 981
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 523643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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2.5e+02;
ches 72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 34.8; DB
Pred. No. 18;
0; Mismatches
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4.2%; Score 34.8; D
Best Local Similarity 52.0%; Pred. No. 2.5e
Matches 78; Conservative 0; Mismatches
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                                           PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR PLILING DATE: 2000-11-30
PRIOR PLILING DATE: 2001-01-06
PRIOR PLILING DATE: 2001-01-16
PRIOR PLILING DATE: 2001-01-06
PRIOR FILING DATE: 2001-01-06
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FREUSEQ for Windows Version 4.0
APPLICATION NUMBER: US 60/243,096
FILING DATE: 2000-10-24
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; LCCATION: (1)...(523643)
; OTHER INFORMATION: n = A,T,C or G
US-10-330-773-308
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Best Local Similarity 51.3%;
Matches 81; Conservative
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APPLICANT: David W. Morrie
APPLICANT: Marc Malandro
                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-3542
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ORGANISM: Homo sapiens
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LENGTH: 904
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                                                                                                                                                                                                                                                             APPLICANT: Wang, David G. TITLE OF INVENTION: Identification and Mapping of Single TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION WHERE: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
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40125 TATGTACCCTTCATCTTCCTTTAATA 40154
                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NULLECLING CAST TITLE OF INVENTION: NULLECLING CURRENT APPLICATION NUMBER: US/09/925,065A CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR PILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/25,147
PRIOR APPLICATION NUMBER: US 60/25,147
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 95/086
SOFTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 630175
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Pred. No. 16;
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Publication No. US20040181048A1
GENERAL INFORMATION:
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Publication No. US20040181048A1
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Best Local Similarity 45.9%;
Matches 150; Conservative
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US-09-925-065A-630175
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314 GATCATTATTACCATGATGTTAAATATGATTTTGTTTAATTATGCTAAGCACTTCATAT 373
                                                                              379 AGACAAAAACAGTGTAGAAGCCGTATAAGCATTAA 413
                                                                                                                             374 GCACAACCATACTTTCTATTATTCTATGTTGTAA 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          194 ATATTCATGACTATTGACTTCAGATTATTCATAACCTAAGTAAAAATGTGAAAATACTTC 253
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IITLE OF INVENTION: Identification and Mapping of Single
IITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
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CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
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Pred. No. 16
          PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR PLING DATE: 2000-11-20
PRIOR PLING DATE: 2000-11-20
PRIOR PPLICATION NUMBER: US 60/250,092
PRIOR PLILING DATE: 2000-11-30
PRIOR PLILING DATE: 2001-01-16
PRIOR PLILING DATE: 2001-01-16
PRIOR PLILING DATE: 2001-01-16
PRIOR PLILING DATE: 2001-05-09
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SOFTWARE: FastSEQ for Windows Version 4.0
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LENGTH: 529
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PRIOR APPLICATION NUMBER: US 60/261,766
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APPLICATION NUMBER: US 60/289,846
FILING DATE: 2001-05-09
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Best Local Similarity 47.4%;
Matches 102; Conservative
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Best Local Similarity 55.7%;
Matches 64; Conservative
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US-09-925-065A-487029
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US-09-925-065A-192068
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SEQ ID NO 487029
LENGTH: 419
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RESULT 1
US-08-581-148C-30
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3750, A
                                                                                                                               (without alignments)
5319.757 Million cell updates/sec
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3, Appl:
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Sequence 1
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Sequence 1:
Sequence 10
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                                                                                                          March 5, 2006, 08:22:14 ; Search time 275 Seconds
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/H_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/RE_COMB.seq:*
/cgn2_6/ptodata/1/ina/RE_COMB.seq:*
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Maximum Match 100%
Listing first 45 summaries
                                                                     OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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Query
Match Length DB
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823
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Perfect score:
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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Seguence	Seguence	Sequence						
US-09-949-016-12412	US-09-949-016-131416	US-09-949-002-3239	US-09-949-002-7323	US-09-949-016-12004	US-09-949-016-13041	US-09-949-002-663	US-09-949-002-772	US-09-949-016-11817	US-09-949-016-15439	US-09-949-016-12776	US-09-949-016-15940	US-09-949-016-13631	US-09-949-016-16858	US-09-949-016-12545	US-09-949-016-13546	US-09-949-016-15096	US-09-949-016-64741	US-09-949-016-90120	US-09-806-708B-22	US-09-949-016-108444
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4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.0	4.0	4.0	4.0	4.0	4.0	0.	4.0	4.0
33.6	33.4	33.4	33.4	33.4	33.4	33.4	33.4	33.4	33.4	33.4	33.4	33.2	33.2	33.2	33.2	33	32.8	32.8	32.8	32.6
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LOCATION:
US-09-097-319A-1
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                                                                                                                                                           61 TAAAACATGTGTGTTTACCATTGTATCAATCAGAACATTCAATAAATTAAAGTGA 120
                                                                                          1 CTGCACGGTACTCCAAGTATAAGACACAGCTAAAACACACATAATGCAGTGGTCATGTC
                                                             Gaps
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IITLE OF INVENTION: Regulatory Sequences for Transgenic Plants
NUMBER OF SEQUENCES: 59
                         Score 227; DB 3; Length 6343;
Pred. No. 3.3e-65;
0; Mismatches 15; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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Armstrong, Katherine
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NAME: Stuart, Donald R
TELECOMMUNICATION INFORMATION
TELEPHONE: 317 337 4816
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Hopkins, Nicole
Menke, Michael A.
Pareddy, Dayakar
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                             Query Match
Best Local Similarity 93.9°
Matches 247; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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MEDIUM TYPE: Floppy
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Indiana
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US-08-581-148C-30
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TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: DOWELAND CORRESSEE: DOWELAND 
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Pred. No. 3.4e-59;
0; Miematches 23
LOCATION: 4201..4425
OTHER INFORMATION: /product= "Peroxidase"
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Belmar, Scott
Folkerts, Otto
Hopkins, Nicole
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Best Local Similarity 90.1%;
Matches 236; Congervative
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1595 ACACCCATTGTACATGCTCTTA 1616

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1402 TGCACAGTACTCCCAAGTATAAGACACAACTAAAAACACAACATAATAATACAGTGGTTATA 1461
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                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Woosley, Aaron
TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants
NUMBER OF SEQUENCES: 59
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COMPUTER READABLE FORM:
MEDIUM TYEER PLOPBY disk
COMPUTER: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: PACENTER: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,319A
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                                                                                    Sequence 15, Application US/09097319A
Patent No. 6384207
GENERAL INPORMATION:
APPLICANT: Ainley, Michael
APPLICANT: Armstrong, Katherine
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Belmar, Scott
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Menke, Michael A.
Pareddy, Dayakar
Petolino, Joseph I
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NAME: Stuart, Donald R
TELECOMUNICATION INFORMATION:
TELEPHONE: 317 337 4816
TELEFAX: 317 337 4816
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Matches 236; Conservative
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LENGTH: 9299 base pai
TYPE: nucleic acid
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STATE: Indiana
COUNTRY: USA
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MOLECULE TYPE: DNA
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                                                                    JS-09-097-319A-15
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25.4%; Score 209.2; DB 3; Length 6550;
Best Local Similarity 90.1%; Pred. No. 3.4e-59;
Matches 236; Conservative 0; Mismatches 23; Indels 3;
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..6068)
                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/643,971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: exon
LOCATION: 4201..4425
OTHER INFORMATION: /product= "Peroxidase"
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NAME: Stuart, Donald R
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317 337 4846
TELEPAX: 317 337 4847
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6550 base pairs
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5059..5250
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5251..5382
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5383..5548
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       intron
4426..5058
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5549..5649
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                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                         FILING DATE:
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LOCATION:
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LOCATION:
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NAME/KEY:
LOCATION:
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US-09-643-971-1
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NAME/KEY:
LOCATION:
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LOCATION:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                APPLICANT: Woosley, Aaron
TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3; Length 9299;
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Best Local Similarity 90.1%; Pred. No. 4.2e-59;
Matches 236; Conservative 0; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                     STREET: 9310 Zionsville Road CITY: Indianapolis STATE: Indiana
1642 ACACCCATTGTACATGCTCTTA 1663
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APPLICANT: Armstrong, Katherine
APPLICANT: Belmar, Scott
APPLICANT: Folkerts, Otto
APPLICANT: Polkerts, Nicole
APPLICANT: Pareddy, Dayakar
APPLICANT: Pareddy, Dayakar
APPLICANT: Smith, Kelley
APPLICANT: Smith, Kelley
APPLICANT: Woosley, Aaron
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                            Sequence 15, Application US/09643971
Patent No. 6699984
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NAME: Stuart, Donald R
TELECOMUNICATION INFORMATION:
TELEPHONE: 317 337 4816
TELEFAX: 317 337 4847
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 9299 base pairs
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STRANDEDNESS: double
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
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                                                                                                                                       GENERAL INFORMATION:
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1642 ACACCCATIGIACAIGCICITA 1663

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1468 İCTABARCATGIGICTTACCATATTCATTGTACCAATTAGAAÇATTTAATAATTAAAGT 1527
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                                                                                                                                                                                                                                                  APPLICANT: Woosley, Aaron
TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 3; Length 9408;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,319A
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Pred. No. 4.3e-59;
0; Mismatches 23
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Sequence 16, Application US/09097319A
Patent No. 6384207
                                                                    Ainley, Michael
Armstrong, Katherine
Belmar, Scott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Stuart, Donald R
TELECOMUNICATION INFORMATION:
TELEPHONE: 317 337 4816
TELEFAX: 317 337 4847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 9408 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 90.1%;
Matches 236; Conservative (
                                                                                                                                     Folkerts, Otto
Hopkins, Nicole
Menke, Michael A
Pareddy, Dayakar
Petolino, Joseph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
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APPLICANT: Navarro, Pedro
TITLE OF INVENTION: Antimicrobial Peptides and Methods of
TITLE OF INVENTION: Antimicrobial Peptides and Methods of
TITLE OF INVENTION: Use
FILE REFERENCE: 35118/238472
CURRENT APPLICATION NUMBER: US/09/950,933A
CURRENT PILLING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: 60/232,569
NUMBER OF SEQ ID NOS: 99
SEQ ID NOS: 99
SEQ ID NOS: 99
LENGTH: 720
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Sequence 8, Application US/09950933A Patent No. 6875907
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LOCATION: (119)...(403)
US-09-950-933A-8
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ORGANISM: Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Woosley, Aaron
TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25.4%; Score 209.2; DB 3; Length.9408; 90.1%; Pred. No. 4.3e-59; Indels 3; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/643,971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3: DowElanco Patent Department
9330 Zionsville Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1648 ACACCCATTGTACATGCTCTTA 1669
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                                                                                                                                                                                                            Ainley, Michael
Armstrong, Katherine
Belmar, Scott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Stuart, Donald R
TELECOMMUNICATION INFORMATION:
TELEFAK: 317 337 4816
TELEFAK: 317 337 4847
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Petolino, Joseph
Smith, Kelley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: Floppy disk COMPUTER: IBM PC compatil COBEATING SYSTEM: PC-DO-SOFTWARD SOFTWARD SOF
                                                                                                                                                                                                                                                                                                                                                                        Folkerts, Otto
Hopkins, Nicole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 90.1
Matches 236; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 46268
COMPUTER READABLE FORM:
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STREET: 93
CITY: Indi
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Sequence 160080/c

is Sequence 160080, Application US/09949016

sequence 160080, Application US/09949016

patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR PELING DATE: 2000-10-30

PRIOR FILING DATE: 2000-10-30

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-08

SOFTWARE FREEEROF FOR WINDOWS VERSION 4.0

SOFTWARE FREEEROF FOR WINDOWS VERSION 4.0

SEQ ID NO 160080 61 TAAAACATGTGTCTTACCATATTCATTGTATCAATCAGAACATTCAATAAATTAAAGTGA 120 638 TAAAACATGTGTCTTACGATATTCATTGTACCAATCAGAGTATTCAATAAATTAAAGTGA 697 246 TIGIACAIGCCCIAACIGGCACCGCIACGIAGGGGCTAIICAAGAACCAACCAIGIACAG 305 Gaps ö Length 720; Query Match 5.1%; Score 41.6; DB 3; Length 6 Best Local Similarity' 53.8%; Pred. No. 0.0027; Matches 86; Conservative 0; Mismatches 74; Indels Indela

us-10-660-208-90.rni

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PRIOR FILING DATE: ZUVULL NUMBER OF SEQ ID NOS: 207012 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 15844
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OTHER INFORMATION: n = A,T,C or G
US-10-427-923-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/10427923
Patent No. 6916643
GENERAL INFORMATION:
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Best Local Similarity 49.2%;
Matches 98; Conservative
                                                                                                                                                                                                                                    llarity 48.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
                                                                                                                                                                                                                                      Local Similarity
                                                                                                                            TYPE: DNA
ORGANISM: Human
                                                                                                                                                                       US-09-949-016-15844
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APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PLILNG DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: 10/09/949,016
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-00-00-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTGTTGCAACGTGAATGGTTATTTGCTTCAGATTAAAGCTAATTATTTAGACTGATGCAG 365
                                                          TIGITGCAACGIGAATGGTTATTTGCTTCAGATTAAAGCTAATTATTTAGACTGATGCAG 365
                                                                                                     181 Tricica arriccitatria cranica accarrica carria cara cranica caracterica con 122
              241 TTCTCAAGGATAAAACTGGGACCAATATGGCAGGCAAATTGAAGAACTTGCCTTGTGAGA 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32437 ATGAGATTCTTTCAGTGAAGAAGTAGTAGAGGAGGTTAAA 32398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     366 CTGCAATTCATAGAGACAAAAACAGTGTAGAAGCCGTATA 405
                                                                                                                                                 366 CTGCAATTCATAGAGACAAAAACAGTGTAGAAGCCGTATA 405
                                                                                                                                                                                            121 Argagarrerreagraaaaaaaaagragagagraaa 82
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16222
                                                                                                                                                                                                                                                                              i-09-949-016-16222/c
Sequence 16222, Application US/09949016
Patent No. 6812339
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Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: misc_feature
; LOCATION: (1)...(43562)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 53.8
Marches 86; Conservative
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19119 Taalaalaalaadacacagalaaccretraaccritaterracateaaaackeregere 19178
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TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

FILE REFERENCE: CL001365

CURRENT APPLICATION NUMBER: US/10/427,923

CURRENT FILING DATE: 2003-05-02

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                 436 GCTACAACCAATTTGCTGGGCTTCCATGGGCATCGCAGAAGTATTGTGGCTGCATATTGC
                                                                                                                                                                                                                                                                                                                                                4 CACGGTACTCCAAGTATAAGACACAGCTAAAACACAAACATAATGCAGTGGTCATGTCTAA
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                                                            Gaps
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Length 68580;
                                                                                                               376 TAGAGACAAAAACAGTGTAGAAGCCGTATAAGCATTAAGCAAACAAGCGA
                                                         0; Mismatches 111, Indels
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   Score 38.4; DB 3;
Pred. No. 0.62;
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Length 112222;

DB 3;

Score 37.4; Pred. No. 1.

0; Mismatches 101; Indels

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64 AACATGTGTCTTACCATATTCATTGTATCAATCAGAACATTCAATAAATTAAAGTGACCA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                124 ATCAGATAGTCTCCTGTCCCGAATATAGAGCTAAGACACTGTGTCTTCGTCAAGATACAT 183
                                                                                                                                                                                                                                                4 CACGGTACTCCAAGTATAAGACACCTAAAACACAACATAATGCAGTGGTCATGTCTAA 63
                   | FEATURE:
| NAME/KEY: misc feature
| LOCATION: (1)...(112222)
| OTHER INFORMATION: n = A,T,C or G
| US-09-949-016-14324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184 GTCTTGAGATTTTTTACAT 202
                                                                                                                                                        49.28;
                                                                                                                                                                             Best Local Similarity 49.2
Matches 98; Conservative
ORGANISM: Human
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ORGANISM: Human
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FILE REFERENCE: CLOOD1307

CURRENT APPLICATION NUMBER: 05/241,755

PRIOR PILING DATE: 2000-10-20

PRIOR PELING DATE: 2000-10-20

PRIOR PELING DATE: 2000-10-03

PRIOR PELING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 12453

LENGTH: 112219
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 AACATGTGTCTTACCATATTCATTGTATCAATCAGAACATTCAATAAATTAAAGTGACCA 123
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 14124
LENGTH: 112222
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Pred. No. 1.
                                                           Sequence 12453, Application US/09949016
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; LOCATION: (1)...(112219)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12453
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Best Local Similarity 49.2%;
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Human
FEATURE:
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DETECTION AND USES THEREOF
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4.5%; Score 37.4; DB 3; Length 1
Best Local Similarity 49.2%; Pred. No. 1.8;
Matches 98; Conservative 0; Mismatches 101; Indels
                                                                                                                                                                                                         Sequence 17572, Application US/09949016
Fatent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSITICAE OF INVENTION: WITH HUMAN DISEASE, METHODS OF INTIE OF INVENTION: WITH HUMAN DISEASE, METHODS OF INTIE OF INVENTION: WITH HUMAN DISEASE, METHODS OF INTIE REFERENCE: CLOO1307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241, 755
PRIOR PELICATION NUMBER: 60/241, 756
PRIOR APPLICATION NUMBER: 60/231, 498
PRIOR APPLICATION NUMBER: 60/231, 498
PRIOR FILING DATE: 2000-10-03
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60755 ATCACATAGTATATATAT 60773
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Search completed: March 5, 2006, 08:57:49 Job time : 278 secs

us-10-660-208-90.rni

	Copyright (	GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.	n 5.1.7 Bioccelera	ion Ltd.	
OM nucleic - nucleic search, using sw model	leic search,	using sw model			
Run on:	March 5, 200	March 5, 2006, 10:15:23 ; Search time 4128 Seconds (without alignments) 9327:948 Million cell up	Search time (without alid	Search time 4128 Seconds (without alignments) 9327.948 Million cell updates/sec	
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Total number of hits satisfying chosen parameters:	hits satisfyi	ng chosen param	eters:	82156650	
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

CG011145 ZUAGI45TH
BZ81859 PUFAMBZTB
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CG3131420 CMBK4TTV
CW009430 ZWMBLA001
CG175756 PUJBYZ0TD
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BZ917308 PUGCL66TB BZ795967 PUFFF13TD CW01489 ZWMBLC000 CL984622 ZWMBHG000 CG119014 PUJBF49TB BZ993151 PUDDG29TD BZ992817 PUDDG29TD CG13020 PUKDM45TB CG13020 PUKDM45TB CZ915233 4013010E1 CG065264 PUFPO72TD CW000997 ZWMBHG000 CC002788 PUDHJ3ZTD BZ791746 PUFHN12TD CW018123 ZWMBLG001 CW018123 ZWMBLG001 CW018123 ZWMBLG001	B2994616 PUGGN06TD CG038335 PULJF77TB CG14450 PUFKY41TD CG041190 PUTDN37TB CG107530 PULLN19TD BH234262 1006178D0
BZ817308 BZ795967 CW014489 CD84622 CG119014 BZ992817 CC780832 CG15233 CG065264 CW0100997 CC002788 BZ791746 CW018123	B2994616 CG038335 CG144450 CG043190 CG107530 BH234262
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985 773 687 1118 635 875 875 905 1010 1030 830 621 733	7772 7722 7720 1043 854 448
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## ALIGNMENTS

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Database

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	CG011145 CG011145 CG011145 CG011145 CG011145 CG011145 CG011145 CG011145 CG011145 CG011145 CG01	CG011145 GI33883311		Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.	Consortium for Maize Genomics Unoublished (2002)	Other_GSSs: ZUAGI45TV Contact: Cathy Whitelaw	110s. 712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843 Fax: 101-838-0708	Email: whitelaw@tigr.org Seq primer: TR Class: sheared ends.		/organism="Zea mays" /mol_type="genomic_DNA" /strain="B73" /db xref="taxon:4577" /clone="ZMMBPa0060H17" /clone lib="ZM 3.0 4.0 KB" /note="Vector: pBCSK-; Site_1: HincII; 3-4 kb 'unfiltered'		Query Match 68.5%; Score 564; DB 10; Length 901; Best Local Similarity 99.1%; Pred. No. 1.7e-156; Matches 567; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
RESULT 1 CG011145	LOCUS	ACCESSION VERSION.	SOURCE	AUTHORS	TITLE	COMMENT	•		FEATURES Source		ORIGIN	Query Match Best Local Matches 56

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BZB18600
PUFAM82TD ZM 0.6_1.0_KB Zea mays genomic clone ZMMBTa275M19,
genomic survey sequence.
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1 (bases 1 to 854)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennetzen, J.
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Location/Qualifiers
1. 0854
/ organism="Zea mays"
/ mol type="genomic DNA"
/ strain="B73"
/ db zres="zwMBTa275M19"
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CoT selected genomic DNA library"
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Pred. No. 9e-65;
0; Mismatches. 21; Indels 0;
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Unpublished (2003)
Other GSSs: PUFAM82TB
Contact: Cathy Whitelaw
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Seg primer: TF
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                                                                                                                     Query Match
Best Local Similarity 92.8%;
Matches 269; Conservative
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Fax: 301-838-0208
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PUFFAM82TB ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa275M19,

BZ818599
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
                                                                          201 TTCATAGAGACAAAAACAGTGTAGAAGCCGTATAAGCATTAAGCAAACAAGAGGGAACATTG
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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
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/mol_type="genomic DNA"
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Class: sheared ends.
Location/Qualifiers
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Unpublished (2003)
Other GSSs: PUFAM82TD
Contact: Cathy Whitelaw
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Fax: 301-838-0208
Email: whitelaw@tigr.org
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FEATURES

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CW009430 847 bp DNA linear GSS 23-SEP-2004
ZMMBLa0012C07.r ZMMBLa Zea mays genomic clone ZMMBLa0012C07 3',
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      178 TAAAACATGTGTCTTGCCATATTCATTGTACCAATCAGAACATTCAATAAATTAAAGTGA 237
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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                                                                               238 ccaarcagaragrerecrerereaararagageraagacacrerereregeragara
                                                                                                                           167 CCAATCAGATAGTCTCCTGTCTCGAATATAGAGCTAAGACACTGTGTCTTCGTCAAGATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        University of Arizona
Forbes Bullding Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
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Wing, R., Luo, M., Soderlund, C. and Haller, K.
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/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: rwing@genome.arizona.edu
Plate: 0012 row: C column: 07
Class: BAC ends.
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Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
                                                                                                                                                                                                                                              358 ACCCACTGTACATGCCCTAA 377
                                                                                                                                                                                                                                                                                                                                                                                          yenomic survey sequence.
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Best Local Similarity
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CW009430
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
Contact: Cathy Whitelaw
                                                                                                                                                                     111 TAAAACATGTGTCTTACCATATTCATTGTACCAATCAGAACATTCAATAAATTAAAGTGA
                                                                                                      771 CTGCACGGTACTCCAAGTATAAGACACAGCTAAAACACACATAATACAGTGGTCATGTC
                                                                                                                                           61 TAAAACATGTGTCTTACCATATTCATTGTATCAGAACATTCAATAAATTAAAGTGA
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                           0; Gaps
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/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                                          241 ACCCATTGTACATGCCCTAACTGGCACCGCTACGTAGGGGCTATTCAAGA 290
                                                                                                                                                                                                                                                                                                                                                                                                               Length 679;
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                                                              CTGCACGGTACTCCAAGTATAAGACACAGCTAAAACACAACATAATGCA
9e-65;
~hes 21; Indels
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                      0; Mismatches
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        Pred. No.
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Class: methylation filtered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC331420
CC331420.1 GI:30800591
      92.8%;
      Best Local Similarity 92.89
Matches 269; Conservative
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Zea mays
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CW007582 13-SEP-2004 CW007582 CWBLa0009E11,r ZMMBLa Zea mays genomic clone ZMMBLa0009E11 3',
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/organism="Zea mays"
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                                       genomic survey sequence.
                                                                       GI:52588391
                                                                           CW007582.1
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Zea mays
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CW006373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAAAACATGTGTCTTACCATATTCATTGTATCAATCAGAACATTCAATAAATTAAAGTGA 120
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COT selected genomic DNA library"
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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
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Best Local Similarity 93.9%; Pred. No. 2.1e-63;
Matches 262; Conservative 0; Mismatches 17; Indels 0;
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Fax: 301-838-0208
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                          241 ACCCATTGTACATGCCCTAACTGGCACCGCTACGTAGGG 279
                                             287 ACCCATTGTACATGCCCTCATACGCACTTCGCAGTGCGG 325
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Class: sheared ends.
Location/Qualifiers
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Unpublished (2003)
Other GSSs: PUJBY20TB
Contact: Cathy Whitelaw
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Zea mays
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RESULT 7 CW007582

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REFERENCE AUTHORS

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ZMMBLa0007D24.f ZMMBLa Zea mays genomic clone ZMMBLa0007D24 5', genomic survey sequence. CW006373 CW006373.1 GI:52585956
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCAATCAGATAGTCTCCTGTCCCGAATATAGAGCTAAGACACTGTGTCTTCGTCAAGATA 180
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1 (bases 1 to 695)
Wing,R., Luo,M., Soderlund,C. and Haller,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism: may bow."
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/mol type="genomics DNA"
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                                                                                                                     ZMMBL sequences
Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: $20 625 9595
Email: rwing@genome.arizona.edu
Plate: 0009 row: B column: 11
Class: BAC ends.
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30.4%; Score 250.4; DB 10; Length
Best Local Similarity 97.7%; Pred. No. 5.3e-63;
Matches 254; Conservative 0; Mismatches 6; Indels
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Contact: Cathy Whitelaw
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CC607552 902 bp DNA linear GSS 18-JUN-2003 OGUBNGOTV ZM 0.7_1.5_KB Zea mays genomic clone ZMMBMa0401J24, genomic survey sequence.
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1 (Dases 1 to 902)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing; T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGUBN60TH
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30.4%; Score 250.4; DB 10; Length 777;
Best Local Similarity 97.7%; Pred. No. 5.5e-63;
Matches 254; Conservative 0; Mismatches 6; Indels 0;
                                                                                                                                                                                                                                                                                                                   /organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
                                                                                                                                                                                                                              Email: rwing@genome.arizona.edu
Plate: 0007 row: D column: 24
Class: BAC ends.
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735 bp DNA linear GSS 25-MAR-2003
PUGRN02TB ZM 0.6_1.0 KB Zea mays genomic clone ZMWBTa372B04,
genomic survey sequence.
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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/clone_lib="ZM_0.7 1.5_KB"
/note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 kb
methylation filtered genomic_DNA library"
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9712 Medical Center Drive, Rockville, MD 20850, USA
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Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.
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                                                                                                                                                                                                                                                      /organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
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Class: methylation filtered.
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                                                      Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
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Other_GSSs: PUGFN02TD
Contact: Cathy Whitelaw
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Class: fosmid ends.
Location/Qualifiers
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Best Local Similarity 96.2
Matches 255; Conservative
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Ma,J., SanMiguel,P., Liu,R., Haller,K., Soderlund,C. and Bennetzen,J.
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CoT selected genomic DNA library"
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Unpublished (2004)
Contact: Jeff Bennetzen
Bennetzen Lab
The University of Georgia
Department of Genetics, C426a Life Sciences Building, Athens, GA
                                                                                                                                                                                                                              Gaps
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Plate: 0001 row: n column:
Class: BAC ends.
                               'organism="Zea mays"
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Fax: 706-583-0972
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Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 893)
Bharti, A.K., Nelson, A.B., Young, S., Keizer, G., Zohovetz, V., Fuks, G. and Messing, J.
Construction, Sequencing and Characterization of a Fosmid Library of the B73 Maize Genome
Unpublished (2005)
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ZMMBF0140018r ZMMBF Zea mays genomic clone ZMMBF0140018 3', genomic
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Dr.Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 CCAATCAGATAGTCTCCTGTCCCGAATATAGAGCTAAGACACTGTGTCTTCGTCAAGATA 180
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190 Frelinghuysen Road, Piscataway, NJ 08854, USA
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96.2%; Pred. No. 1.5e-62;
iive 0; Mismatches 10;
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Fax: 732 445 5735
Email: bhartl@waksman.rutgers.edu
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CC397968 717 bp DNA linear GSS 19-MAY-2003 PUHDC37TD ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa424G01,
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Zea mays
Lokaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
(Passes 1 to 717)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
  213 TAAAACATGTGTCTTACCATATTCATTGTACCAATCAGAACATTCAATAAATTAAAGTGA 154
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                                                                                                                                                            93 CATGICTIGAGATTITITIACATITCACCCCCTAGACACACTCTAAGACACACATTAAAGA 34
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Fax: 301-838-0208
Email: whitelaw@tigr.org
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Other GSSs: PUHDC37TB
Contact: Cathy Whitelaw
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  Pred. No. 1.7e-
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Unpublished (2003)
Contact: Cathy Whitelaw
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hitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
tesnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
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Unpublished (2003)
Other GSSs: PUHDC37TD
Contact: Cathy Whitelaw
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Seg primer: TR
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Adx61698
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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	ALIGNMENTS				•		
Adx12232 Plant ful	ADX12232	13	398	. j	41.8	45	
Maize	ADQ04636	12	281	5.1	41.8	44	
Maize	ADQ04637	12	264	5.1	41.8	43	
	ADX29247	13	527	5.1	42.2	42	
Adx64747 Plant ful	ADX64747	Ξ	2109	5.3	43.4	41	
	AAC51726	ო	2025	5.3	43.4	40	U
Ada71938 Rice gene	ADA71938	œ	2000	5.3	43.4	33	
Plant	ADX62639	13	1807	5.3	43.4	38	U
	ADX63325	7	1707	5.3	43.4	37	U
	ADX60046	13	1699	ŭ.	43.4	36	U
	ADM47884	12	1696	5.3	43.4	35	υ
Adx62396 Plant ful	ADX62396	13	1676	5.3	43.4	34	U
	AD083107	13	1272	5.3	43.4	33	_
	ADX35171	13	1184	5.3	43.4	32	
Plant	ADX34170	13	891	5.3	43.4	31	
Plant	ADX10043	13	377	5.3	43.4	30	0
Maize	ADQ04600	12	271	5.3	43.4	53	
Plant	ADX48874	=	1538	5.4	44.2	28	о 
Plant	ADX52319	13		5.4	44.2	27	_
	AD083991	13		5.4	44.2	26	
tion (2	ADQ97047 1	12	110000	5.4	44.6	25	0
Plant	ADX46949	13	1412	5. 8.	47.6	24	
Plant	ADX33856	13	781	6.0	49	53	
	ADX52602	H	2074	6.1	9:05	22	U
	ADX33788	n	505	6.1	50.6	21	
Ado83463 Plant ful	ADO83463	13	1318	6.5	53.6	20	·

Corn; male reproductive tissue; plant regulatory sequence; Zea mays; promoter; transcription regulation; operably linked gene; monocot; dicot; wheat anther; plant fertility; insect tolerance; pathogen tolerance; herbicide tolerance; ds. AAS96569 standard; DNA; 823 BP Corn promoter sequence #12 26-FEB-2002 (first entry) AAS96569 AAS96569 

Zea mays

WO200183790-A2

08-NOV-2001

30-APR-2001; 2001WO-US013739.

(MONS ) MONSANTO TECHNOLOGY LLC 01-MAY-2000; 2000US-0201255P.

Magucci JD; Malven M, Dubois P, Conner TW,

WPI; 2002-055481/07.

Novel promoters isolated from corn for controlling gene expression in male reproductive tissues, such as anthers, tassels, and to regulate transcription of target genes including genes for insect or pathogen tolerance

Claim 1; Page 113-114; 121pp; English.

The present invention relates to the isolation of plant regulatory sequences from the male reproductive tissues of corn (Sea mays). The promoter sequences, fragments, regions or cis elements of the sequences, are capable of regulating transcription of an operably linked DNA

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sequence. The promoter sequences confer enhanced expression of operably linked genes in monocot or dicot male reproductive tissues, such as anthers, especially wheat anthers and is useful for regulating transcription of a DNA sequence, by operably linking the DNA sequence to transcription of target genes including genes for control of fertility, insect or pathogen tolerance and herbicide tolerance. They are also useful as probes or primers in nucleic acid hybridisation experiments. The promoter sequences can be used in hybridisation assays of other plant tissues to identify closely related or homologous genes and associated regulatory sequences. AAS96558 AAS96577 represent the corn promoter
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; Pred. No. 9.9e-256;
0; Mismatches 0;
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Best Local Similarity 100.
Matches 823; Conservative
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The present invention relates to the isolation of plant regulatory sequences from the male reproductive tissues of corn (Zea mays). The promoter sequences, regions or cis elements of the sequences, are capable of regulating transcription of an operably linked DNA sequence requences confer enhanced expression of operably linked GNA anthers, especially wheat anthers and is useful for regulating contractive tissues, such as anthers, especially wheat anthers and is useful for regulating the DNA sequence. The promoter sequences are useful in plants to regulate transcription of target genes including genes for control of fertility. Insect or pathogen tolerance and herbicide tolerance. They are also useful as probes or primers in nucleic acid hybridisation assays of other plant tissues to identify closely related or homologous genes and associated tissues to identify closely related or homologous genes and associated transcription.
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1412 GCCAAGCCGAGCCGGTCGTCCGTCCAACCCCCCTCGTTTATACTATATACACAGA 1471
                                                                                                                                                                                                                                                                                                         1472 CGCACGATACCCATATCGTGGTGCTAGAAGCAACTGAAAACAGCCGAGCGATCTCCTCTC 1531
                                                               CTTAGCTACAACCAATTTGCTGGGCTTCCATGGGCATCGCAGAAGTATTGTGGCTGCATA 1231
                                                                                                              491
                                                                                         551
                                                                                                                                        611
                                                                                                                                                                                         671
                                                                                                                                                                                                                                           731
                                                                                                                                                                                                                                                                                          732 CGCACGATACCCATATCGTGGTGCTAGAAGCAACTGAAAACAGCCGAGCGATCTCCTCTC 791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactoromannan production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield; protein content; gene; se.
                                                                                                                                                                                        612 GTCAACATGCCTGGATCCACGGGGAGCGAGGAGACGAATGTGTGGCCCGCCGCCGCAGTGAG
                                                                                       TTGCTGAAATTATAGCGAGGGCCCAAGGCCCATCACTTCACTTCGAGGTCAGCATTGTAC
                                                                                                                                       TITIGITAACGICICGATAAATTIGITCACTTAAAATAGACCAGTTCAATTCTGGTTCTA
                                                                                                                                                                                                                                           GCCAAGCCGAGCCCGGTCGTCCGTCCACCCCCTCGTTTATACTATATACAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cao Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tabaska JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plant full length insert polynucleotide segid 22826.
                                                                                                                                                                                                                                                                                                                                                         1532 CCTCTCCCTCTCCGATCCATTCTCCAGCGCAG 1563
                                                                                                                                                                                                                                                                                                                                            CCTCTCCCTCTCCGATCCATTCTCCAGCGCAG 823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Screen SE,
                                                                                                                                                                                                                                                                                                                                                                                                                               ADX48086 standard; cDNA; 1578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhou Y, Kovalic DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-APR-2003; 2003US-00425114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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TABASKA J E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-180133/17
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(ZHOU/)
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(SCRE/)
(TABA/)
(CAOY/)
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The invention describes a recombinant DNA construct comprising a polymucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at available in electronic form from the US patent office at polymucleotide of the invention are also useful in physical arrays of molecules and as plant breading markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or perss, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, lighin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one content. This sequence represents a plant full length insert content. On the content of the recombinant DNA construct of the polymucleotide that can be used in the recombinant DNA construct of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 ATGTCTTGAGATTTTTACATTCACCCCCCTAGACACCTCTAAGACACACTTAAGACA 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens pests, for conferring increased resistance to plant disease, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Maize, glossy2; gl2; cuticle, cuticular lipid biosynthesis;
lipid composition; lipid quantity; disease resistance; pest resistance;
wind resistance; frost resistance; UV resistance; transgenic plant;
antisense inhibition; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1054 TGCACGGTACTCCAAGTATAAGACACACCTAAAACACAAACATAATACAGTGGACGTGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              994 AAAACATGTGTCTTACCATATTAATTGTACCAATCAGAGCATTCAATAAATTAAAGTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 AAAACATGTGTCTTACCATATTCATTGTATCAATCAGAACATTCAATAAATTAAAGTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 TGCACGGTACTCCAAGTATAAGACACAGCTAAAAACACATAATGCAGTGGTCATGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAATCAGATAGTCTCCTGTCCCGAATATAGAGCTAAGACACTGTGTCTTCGTCAAGATAC
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28.1%; Score 231; DB 13; Length 1:
Best Local Similarity 92.4%; Pred. No. 1.5e-63;
Matches 243; Conservative 0; Mismatches 20; Indels
                                                                                                 Claim 1; SEQ ID NO 22826; 15pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCCATTGTACATGCCCTAACTGG 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCCACTGTACATGCCCTAATCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Maize glossy2 (gl2) gene.
                                                             improving yield.
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09-MAY-2000

Hansen JD;

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The invention relates to transforming a plant cell with either a nucleic acid encoding a plant cuticular lipid biosynthetic protein, or an antisense nucleic acid sequence targetred to a plant cuticular lipid gene, and then generating a plant from the plant cell. The cuticular lipid genes that may be used in the invention are given in AAA57871-A57884 and AAA57891. The cuticular consists of a meshwork (cutin) of cross-seterified polymerised hydroxy-fatty acids embedded in a complex mixture of nonpolar lipids (the cuticular axa). The cuticula protects and strengthens the plants, prevents evaporation of internal fluids and filters UV radiation. Mutations in the cuticular lipid genes affects the quantity and composition of cuticular lipids; in maize, 17 loci (the glossy (gl)) genes) have been identified as being in involved in cuticular lipid sownthesis or control. The method is useful for introducing a nucleic acid into a cell preferably of maize, soybean, rapeseed, canola, cotton, safflower, peanut, palm or sunflower plant and generating a plant from the plant cell. The transformed plants have improved environmental resistance relating to wind, frost, UV or drought; fungal, bacterial or viral disease resistance, september in sequence represents the maize glossy2 (gl2) gene
                                                                                                                                                                                                                                                   Transforming plants such as maize and canola, for producing new plant varieties having disease and pest resistance involves introducing cuticular lipid genes into the plant genome.
                                                                                                                                                            Robertson DS,
                                                                                                                                                               Nikolau BJ, Xu X, Xia Y,
                                                                                                                  (IOWA ) UNIV IOWA STATE RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                    Example 7; Col 115-122; 69pp; English.
                      95US-00581148
                                                                   94US-00218028
                                                                                                                                                                                                           WPI; 2000-349707/30.
                                                                                                                                                                 Schnable PS,
                                                                     24-MAR-1994;
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Sequence 6343 BP; 1493 A; 1667 C; 1607 G; 1564 T; 0 U; 12 Other;

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3675 TAAAACATGTGTCTTACCAIATTTATTGTACCAATCAGGGGATTCAATAAATTAAAGTGA 3734
                                                                                                                                                                                                                                                          3795 CATGTCTTGAGATTTTTTACATTCACCTCCTAGACACACTCTAAGACACAACTTAAGAC 3854
                                                                                                   61 TAAAACATGTGTCTTACCATATTCATTGTATCAATCAGAACATTCAATAAATTAAAGTGA 120
                                                                                                                                                                                                                                                                                                              181 CATGICTIGAGATTTTTACATTCACCCCCTAGACACACTCTAAGACACAACTTAAGAC 240
                                                                                                                                                                                                                                    121 CCAATCAGATAGTCTCCTGTCCCGAATATAGAGCTAAGACACTGTGTCTTCGTCAAGATA 180
                                                                                 9
                                                                               CTGCACGGTACTCCAAGTATAAGACACAGCTAAAACACAACATAATGCAGTGGTCATGTC
                                           1; Gaps
Query Match

27.6%; Score 227; DB 3; Length 6343;
Best Local Similarity 93.9%; Pred. No. 6.6e-62;
Matches 247; Conservative 0; Mismatches 15; Indels
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         Query Match
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Plant full length insert polynucleotide segid 31817.

(first entry)

21-APR-2005

ADX60974;

8×4×4×8

BP

ADX60974 standard; cDNA; 1326

RESULT 5

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61 TAAAACATGTGTGTTTACCATATTCATTCAATCAACATTCAATAAATTAAAGTGA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 CCAATCAGATAGTCTCCTGTCCCGAATATAGAGCTAAGACACTGTGTCTTCGTCAAGATA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent of file at the sequence. The parent of the polynucleotide of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for plant breeding markers. The recombinant DNA construct is useful for plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing glactomanna, lignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or photosynthesis or carbohydrate, nitrogen or photosynthesis or carbohydrate, nitrogen or photosynthesis or carbohydrate, nitrogen or photosynthesis or carbohydrate, nitrogen or photosynthesis or carbohydrate, nitrogen or photosynthesis or carbohydrate, nitrogen or photosynthesis or carbohydrate, nitrogen or photosynthesis or carbohydrate, nitrogen or photosynthesis or carbohydrate, nitrogen or photosynthesis or carbohydrate, nitrogen or photosynthesis or carbohydrate, nitrogen or photosynthesis or carbohydrate, nitrogen or photosynthesis or carbohydrate, nitrogen or photosynthesis or carbohydrate, nitrogen or property or produced the page and or produced the page and or produced the page and or photosynthesis or carbohydrate, nitrogen or produced the page and or produced the page and or produced the page and or produced the page and or produced the page and or produced the page and or produced the page and or produced the page and or produced the page and or produced the page and or produced the page and or produced the page and or produced the page and or produced the page and or produced the page and or produced the page and or
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  plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistence; pest tolerance; yield; plant growth, plant development; seed oil; protein yield; protein content; gene; ss.
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Pred. No. 4.4e-60;
0; Mismatches 23; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   18-APR-2003; 2003US-00425114.
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05-NOV-2001; 2001US-00985678.
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Best Local Similarity 91.1%;
Matches 245; Conservative
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TABASKA J E
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CAOY/) CAO Y.
                                                                                                                                                                                                                                                                       Unidentified.
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(SCRE/)
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Claim 1; Page 84-89; 150pp; English.
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Smith K,
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Pareddy D, Petolino JF,
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                                                                  misc_feature
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4420. .5064
/*tag= o
/note= "this sequence is specifically claimed in Claim 2"
                                                                                                                                                                                                               Peroxidase; per5 gene; maize; corn; transgenic plant; promoter; root; ds.
                                                                                                                                                                                                                                                                                 region is specifically claimed in Claim 1"
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note= "this region is specifically claimed in Claim 1"
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note= "this region is specifically claimed in Claim 1"
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note= "this region is specifically claimed in Claim 1"
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                                                                                                                                                                                             Maize per5 root preferential cationic peroxidase gene.
                                                                  241 ACCCATTGTACATGCCCTAACTGGCACCG 269
                                                                               ACATATTGTACATGCCCTAAGGGGAGTCG 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contains introns"
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product= "peroxidase"
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                                                                                                                                   AAV63717 standard; DNA; 6550 BP.
                                                                                                                                                                                                                                                                        /*tag= a
'note= "this
                                                                                                                                                                                                                                                                                                                                                                                                         .4148
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*tag= b
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187. .
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           254
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This is the nucleotide sequence of the maize per5 root preferential cationic peroxidase gene, which encodes a 333-amino acid peroxidase polypeptide (see AAW8783). Genomic clones comprising per5 sequences were isolated from a maize W22 genomic library using a probe based on isolated from a maize W22 genomic library using a probe based on isolated per5 cDNA. Overlapping subfragments of the gene were sequenced to ger5 cDNA. Overlapping subfragments of the per5 gene. Regulatory sequences derived from the per5 gene, including the promoter, introns and 3 untranslated region (3/UTR), are used in claimed recombinant gene cassettes for controlling expression of recombinant genes in selected itsue, especially the root, of transformed plants, particularly maize. The gene cassettes can be used for expression of heterologous genes such as those that confer tolerance to herbicides, insects or viruees, and genes that provide improved nutritional value or processing characteristics to the plant. Use of the per5 3'UTR sequences provides characteristics to the plant. Use of the per5 3'UTR sequences provides 3'UTR. \*tag= r note= "this sequence is specifically claimed in Claim 2" \*tag= u note= "this sequence is specifically claimed in Claim 2" 542. .5654 /notes "transcription termination sequence, specifically claimed in Claim 3" \*tag= p number= 1 not== "this intron is specifically claimed in Claim 2" (059 q \*tag= q number= 3 note= "this intron is specifically claimed in Claim 2" i650. .6065 \*tag= 8 number= 2 number= this intron is specifically claimed in Claim 2" 383. .5548 \*tag= x note= "this sequence is specifically claimed in Claim 549. 5649 Hopkins N, Menke MA, New isolated regulatory sequences for transgenic plants - which are derived from the maize root preferential cationic peroxidase protein Folkerts O, Woosley A;

us-10-660-208-90.rng

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10-JUN-1998;
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                                    12-JUN-1997;
     17-DEC-1998
                                                                                                                           (per5) gene
                                                                           Pareddy D,
                                                                   Ainley M,
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                                                                   rcraaaacargrerrraccararrcarreraccaarragaacarrraaraaarrraagr 1474
                                                                                                                    178
                                                                                                                                   1475 gaccaarcagcraccracrarcrasacaragagcraagacarrargrarrargacracaraga 1534
                                                                                    118
                                                                                                                                                  TACATGICITGAGATITITIACATICACCCCCTAGACACACTCTAAGACACACTTAAG 238
                                                     28
                                                     2 TGCACGGTACTCCAAGTATAAGACACAGCTAAAACACAACATAATG----CAGTGGTCATG
                                                                                                                                                                                                                                                                                                       Peroxidase; per5 gene; maize; corn; transgenic plant; promoter; root; vector; plasmid PerGUS16; beta-glucuronidase; uidA; reporter gene; ds
                                                                                    GACCAATCAGATAGTCTCCTGTCCCGAATATAGAGCTAAGACACTGTGTCTTCGTCAAGA
                                      Gaps
      Sequence 6550 BP; 1844 A; 1427 C; 1346 G; 1933 T; 0 U; 0 Other;
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note= "per5 promoter and untranslated leader"
248. ,4263
                     DB 2; Length 6550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ct= "beta-glucuronidase"
"Escherichia coli uidA reporter gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         untranslated region from pBI221"
                                      Indels
                                     23;
                     Score 209.2; DB
Pred. No. 4e-56;
0; Mismatches
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/note= "Bluescript II SK-"
                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "per5 exon 1"
264. .6068
                                                                                                                                                                                                1595 ACACCCATTGTACATGCTCTTA 1616
                                                                                                                                                                                   ACACCCATTGTACATGCCCTAA 260
                                                                                                                                                                                                                                                                                                                                                                                    location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note= "nos 3'UTR"
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                     Query Match
Best Local Similarity 90.1%;
Matches 236; Conservative 0
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.6407
*tag= f
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product=
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Agrobacterium tumefaciens
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                              .4247
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                                                                                                                                                                                                                                                                                       Vector plasmid PerGUS16
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                                                                                                                                                                                                                                                                                                                       circular; cyclic.
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This is the nucleotide sequence of PerGUS, a plasmid containing 4 kb of the maize root preferential cationic peroxidase perS gene comprising the perS promoter, untranslated leader, and the first 5 codons of the coding region (i.e. nucleotides 1-4200 of the sequence given in AAV6317), as well as the GUS gene, and the nots 3' untranslated region (3'UTR). It does not include an intron in the untranslated region. The invention relates to new isolated regulatory sequences, especially promoter, intron and 3'UTR sequences, of the maize perS gene. Claimed recombinant gene cassettes comprising perS regulatory sequences are used to control expression of recombinant genes in selected tissue, especially the root, of transformed plants, particularly maize
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCTAAAACATGTGTCTTACCATATTCATTGTATCAGTACATTCAATAAATTAAAGT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 GACCAATCAGATAGTCTCCTGTCCCGAATATAGAGCTAAGACACTGTGTCTTCGTCAAGA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TACATGTCTTGAGATTTTTACATTCACCCCCTAGACACACTCTAAGACACACTTAAG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGCACGGTACTCCAAGTATAAGACACAGCTAAAACACACAACATAATG---CAGTGGTCATG 58
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                                                                                                                                                                                   Menke MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1462 TCTAAAACATGTGTCTTACCATATTCATTGTACCAATTAGAACATTTAATAAATTAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gapa
                                                                                                                                                                                                                                                                                                                                         New isolated regulatory sequences for transgenic plants - which are derived from the maize root preferential cationic peroxidase protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 9299;
                                                                                                                                                                                   Hopkins N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25.4%; Score 209.2; DB 2; Length 90.1%; Pred. No. 4.8e-56; ive 0; Mismatches 23; Indel8
                                                                                                                                                                                   Folkerts O,
Woosley A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 11; Page 108-112; 150pp; Ėnglish.
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Smith K,
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                                                        97US-0049752P
98WO-US011921
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                                                                                                                                                                                      Armstrong K, Petolino JF,
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Best Local Similarity 90.1
Matches 236; Conservative
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1467

28

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1527

178

118

Escherichia coli.

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kb of the maize root preferential cationic peroxidase per5 gene comprising the per5 promoter, untranslated leader, and the first 5 codons of the coding region (1.e. nucleotides 1-4200 of the sequence given in AAV63117), as well as the GUS gene, and the per5 3 untranslated region (3'UTR, i.e. nucleotides 6069-6419 of the sequence given in AAV63117). It demonstrated that the per5 promoter, in the absence of an intron, drives constitutive expression of transgenes in rice. The invention relates to sequences, of the maize per5 gene. Claimed recombinant gene cassettes comprising per5 regulatory sequences are used to control expression of recombinant genes in selected tissue, especially the root, of transformed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This is the nucleotide sequence of PERGUSPER3, a plasmid containing 4.2 kb of the maize root preferential cationic peroxidase per5 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated regulatory sequences for transgenic plants - which are derived from the maize root preferential cationic peroxidase protein
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                                                                                                                                                                           *tag= c
note= "per5 promoter and untranslated leader"
                                                                                                                                                                                                                                                             t= "beta-glucuronidase"
"Escherichia coli uidA reporter gene"
                                                                                                                                                                                                                                                                                                               note= "3' untranslated region from pBI221"
                                                                                                                                                                                                                                                                                                                                                                                       'notes "Bluescript II SK-"
                                                                                                                                              note= "synthetic linker"
                                                                                    .. .42
*tag= a
note= "polylinker site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 12; Page 113-117; 150pp; English
                                                                                                                                                                                                                        note= "per5 exon 1"
                                                                        .ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                        *tag= g
'note= "per5 3'UTR
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Smith K,
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*tag= b
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           Zea mays.
Agrobacterium tumefaciens.
Synthetic.
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Petolino JF,
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                                                                      Key
misc_feature
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Pareddy D,
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                                                Chimeric
                                                                                                                                                             promoter
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1528 GACCAATCAGCTAGCCTCCTGTCTCGAACATAGAGCTAAGACATTGTGTGTCTTCGTCAAGA 1587
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                                                                                                                                                                                                  TACATGTCTTGAGATTTTTACATTCACCCCCTAGACACACTCTAAGACACACATTAAG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for improving yield.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme esmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; land production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield; protein content; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence
                           TGCACAGTACTCCAAGTATAAGACACAACTAAAACACAAAATAATAATACAGTGGTTATA
                                                                                 TCTAAAACATGTGTCTTACCATATTCATTGTATCAATCAGAACATTCAATAAATTAAAGT
                                                                                                 1468 TCTAAAACATGTGTCTTACCATATTCATTGTACCAATTAGAACATTTAATAAATTAAAGT
                                                                                                                                          CTTCGTCAAGA
Gape
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23, Indels
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0, Mismatches
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                                                                                                                                                                                                                                                                        239 ACACCCATTGTACATGCCCTAA 260
                                                                                                                                                                                                                                                                                                                                               ADX49209/c
ID ADX49209 standard; cDNA; 485 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhou Y, Kovalic DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-APR-2003; 2003US-00425114
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05-NOV-2001; 2001US-00985678
                                                                                                                                                                                                                                                                                                                                                                                                                    21-APR-2005 (first entry)
Matches 236; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCREEN S E.
TABASKA J E.
CAO Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KOVALIC D K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-180133/17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unidentified
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Hopkins N, Menke MA;

Folkerts O, Woosley A;

Length 9408;

25.4%; Score 209.2; DB 2; 90.1%; Pred. No. 4.9e-56;

Query Match Best Local Similarity

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the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, lignin or plant. growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert of the
                                                                                                                                                                                                                                                                                                                                                                                                                                   invention
8555555555555555555555
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Sequence 485 BP; 120 A; 126 C; 129 G; 110 T; 0 U; 0 Other;

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422
                                                                                                                            362
                                                                                                                                                    243
                                                                                                   ATCAGATAGTCTCCTGTCCCGAATATAGAGCTAAGACACTGTGTCTTCGTCAAGATACAT 183
                                                                                                                                                                             Grerricadarrirriacarreacececeradacaerereradaeaeaeaerraadaeaeee 302
                                                                 64 AACATGTGTCTTACCATATTCATTGTATCAGAACATTCAATAAATTAAAGTGACCA
                                                                                                                   GTCTTGAGATTTTTACATTCACCCCCTAGACACACTCTAAGACACACTTAAGACACC
                           Gaps
                          .
0
Score 179.4; DB 13; Length 485; Pred. No. 4.3e-47; 0; Mismatches 11; Indels 0;
                                                                                                                                                                                                       CATTGTACATGCCCTAA 260
                                                                                                                                                                                                                                CACTGTACATGCCCTTA 285
  21.8%;
                           Matches 186; Conservative
 Query Match
Best Local Similarity
                                                                              481
                                                                                                      124
                                                                                                                                                                                361
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plant; ss; gene; transgenic; cold tolerance; growth rate; drought tolerance; disease resistance; galactomannan production; plant growth regulator; heat tolerance; herbicide tolerance; lighth production; extreme osmotic condition tolerance; pathogens resistance; pest resistance; yield improvement; seed oil yield;

Corn KCP-like protein encoding DNA, SEQ ID NO

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use invention relates a recombinant with constitute compitating a polypeptide with any of 5544 amino acid sequences (SD44) and encoding any of 5544 untoleotide sequences (SD44) and encoding a polypeptide with any of 5544 amino acid sequences (SD41) No: 5545-11089. The CDNAs and proteins are from corn. soybean, actability of the sequences is derived from which organism. Also included is a method of sequences is derived from which organism. Also included is a method of producing a plant having an improved property, comprising transforming a plant with a recombinant DNA construct comprising a promoter region functional in a plant cell operably joined to a polynucleotide encoding a plant with a recombinant DNA construct comprising a promoter region functional in a plant cell operably joined to a polynucleotide encoding a plant. The property is selected from improving plant cold tolerance, for plant. The property is selected from improving plant cold reseased cresistance to plant disease, for glactomannan production, for production of plant growth regulators, for improving plant tolerance to collaring plant tolerance to extreme osmotic conditions, for improving plant tolerance to extreme osmotic conditions, for improving plant tolerance to extreme osmotic conditions, for improving plant tolerance to extreme osmotic conditions, for improving plant collaring seed protein yield and/or content, for modifying seed protein yield and/or content, for modifying seed protein yield and/or content, for and for yield improvement by providing improved plant growth and development under at least one stress condition. The polymucleotide may also encode a plant transcription factor. The methods and compositions of the present invention are useful in the field of blochemistry and proved introgen collaring the methods and compositions of plants with improved mitrogen plants with improved mitrogen collaring to a plant transcription factor. The methods and compositions of plants with any providing improved methods and composition where 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1088 CAATAAATTAAAGTGACCAATCAGCTAGTCTCCTGTCTCGAACATGAAGTTAAAGTAAGATACTG 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               224
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               New recombinant DNA constructs useful in the field of biochemistry and genetics, and in particular for producing transgenic plants with improved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          flow, increasing plant tolerance to cold or heat, improving plant tolerance to extreme osmotic and drought conditions, and improving plant tolerance to plant pests or pathogens. They can also be used in physical arrays of molecules, plant breeding markers, computer-based storage and analysis systems. The present sequence is one of the 5544 plant cDNA sequences of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1028 TGTCTTCGTC-AGATACATGTCTTGAGTTTTTTTACATTCACCCCCCTAAACACACTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            165 IGTCTTCGTCAAGATACATGTCTTGAGATTTTTTACATTCACCCCCTAGACACACTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105 CAATAAATTAAAGTGACCAATCAGATAGTCTCCTGTCCCGAATATAGAGCTAAGACACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 13; Length 1088;
                                                                                                                                                                                        invention relates a recombinant DNA construct comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1088 BP; 265 A; 261 C; 260 G; 302 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 91.0%; Pred. No. 1.1e-28;
Matches 142; Conservative 0; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              electronic format directly from USPTO at
segdata.uspto.gov/sequence.html?DocID=20040216190.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              225 AGACACAACTTAAGACACCCATTGTACATGCCCTAA 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        969 AATCACAACTTAAGACACTCATTGTACATACCCTTA 934
                                                                                                                                    Claim 1; SEQ ID NO 2967; 14pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAL37816 standard; DNA; 720
                                                genetics, and in particular biological characteristics.
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2×2×2×3
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The invention relates to an isolated polynucleotide encoding a polypeptide which is related to potato snakin antimicrobial protein and GASA4 or GAST1 homologues, which is referred to as lysine- and cysteine- rich peptides (KCP)-like polypeptide, having a nucleotide sequence from 36 sequences of defined base pairs, given in the specification. A recombinant expression cassette comprising the isolated polynucleotide of the invention is useful for modulating the level of (KCP)-like polypeptides is increased, and disease resistance is enhanced. This polypurcleotide sequence represents the DNA encoding a KCP-like protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 TAAAACATGTGTCTTACCATATTCATTGTATCAATCAGAACATTCAATAAATTAAAGTGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    638 raaaacargrictraccararricarricaarccaarcaggrarricaaraarraaagrga 697
                                                                                                                                                                                                                                                                                                                                                                                                                                      New polynucleotide encoding lysine- and cysteine-rich peptides-like polypeptide useful for modulating the polypeptide level in a plant cell,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CTGCACGGTACTCCAAGTATAAGACACAGCTAAAACACAAAATGCAGTGGTCATGTC
                                   GASA4; GASA5; GAST1 homologue; lysine- and cysteine- rich peptide;
KCP-like polypeptide; modulating; disease resistance; gene; ds.
                 potato snakin antimicrobial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 720 BP; 195 A; 215 C; 163 G; 147 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 13.4%; Score 110.2; DB 6; Length Best Local Similarity 90.1%; Pred. No. 1.5e-24; Matches 118; Conservative 0; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plant full length insert polynucleotide segid 27876.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 118-119; 163pp; English.
               Antimicrobial; transgenic; plant;
GASA4; GASA5; GAST1 homologue; lys
                                                                                                                                                                                                                                                                                                                                           Navarro Acevedo PA;
                                                                                                                                                                                                                                                                                                   (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADX53136 standard; cDNA; 737 BP.
                                                                                                                                                                                                                                            13-SEP-2000; 2000US-0232569P.
11-SEP-2001; 2001US-00950933.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            enhancing disease resistance.
                                                                                                                                                                                                      13-SEP-2001; 2001WO-US028429
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P-PSDB; AAO21289.
                                                                                                                           WO200222821-A2
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                                                                                                                                                                                                                                                                                                                                           Simmons CR,
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ADX53136
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New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          672 TAAAACATGTGTCTTACGATATTCATTGTACCAATCAGAGTATTCAATAAATTAAAGTGA 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention describes a recombinant DNA construct comprising a polymucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at the present of the invention are also useful in physical arrays of molecules and as of the invention are also useful in physical arrays of molecules and as lant braceding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactemannan, lightin or plant growth regulators, for increaseling the rate of homologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert polynucleotide that can be used in the recombinant DNA construct of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              614 CTGCACGGTACTCCAAGTACAAGATACAACTAAAACACAAC--AATACAGTGGTCATGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAAAACATGTGTCTTACCATATTCATTGTATCAGAACATTCAATAAATTAAAGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGCACGGTACTCCAAGTATAAGACACAGCTAAAACACAAAATAATGCAGTGGTCATGTC
extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield; protein content; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Таравка ЈЕ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kovalic DK, Screen SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 27876; 15pp; English.
                                                                                                                                                                                                                                                                06-MAY-1999; 99US-00304517.
                                                                                                                                                                                                                           18-APR-2003; 2003US-00425114
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Matches 116; Conservative
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TABASKA J E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             improving yield.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhou Y,
                                                                                                                                               JS2004034888-A1
                                                                                                                                                                                                                                                                                                                                              ZHOU Y
                                                                                                                                                                                                                                                                                                                                                                                                                          CAO Y
                                                                                                           Unidentified
                                                                                                                                                                                       19-FEB-2004.
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99US-0147416P.
99US-014743P.
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990S-0146386P.
99US-0146389P.
99US-0146389P.
99US-0147038P.
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99US-0145087P.
99US-0145192P.
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9905-0139462P
9905-0139750P
9905-0139899P
9905-0149899P
9905-0140538P
9905-0140695P
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990S-0142803P.
990S-0142920P.
990S-0143542P.
990S-0144605P.
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990S-0144066P-
990S-014433EP-
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09-AUG-1999;
10-AUG-1999;
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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic; pathway; promoter; termination sequence; corn; ss.
                                                  Zea mays DNA fragment SEQ ID NO: 40373.
            AAC43750 standard; DNA; 769 BP
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9903-0137724P.
9903-0138540P.
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99US-0123180P.
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99US-012664P.
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                                      18-OCT-2000 (first entry)
                                                                                         Zea mays subsp. mays.
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19-MAY-1999
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                         AAC43750;
 RESULT 13
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9.1%; Score 74.6; DB 3; Length 769;
18.7%; Pred. No. 5.4e-13;
ve 1; Mismatches 0; Indels
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990S-01582329-
990S-01592939-
990S-01592949-
990S-01592349-
990S-01593309-
990S-01593319-
990S-01593319-
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99US-0161920P.
99US-0161992P.
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Matches 74; Conservative
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99US-01577
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749 GIGGIGCIAGAAGCAACIGAAAACAGCCGAGCGATCTCCTTCCCTCTCCCTCTCCGATC 808 809 CATTCTCCAGCGCAG 823 δ

CATTCTCCAGCGCAS 75 61 용

ò g RESULT 14 ADX33652 ID ADX33652 standard; cDNA; 821 BP.

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plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolarance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; pest tolerance; galactoremannan production; ignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield; protein content; gene; ss.
                                                                                                                                                                                                                                                                                                         Cao Y;
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                                           Plant full length insert polynucleotide segid 16472.
                                                                                                                                                                                                               06-MAY-1999; 99US-00304517
05-NOV-2001; 2001US-00985678
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                         (first entry)
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KOVALIC D K.
SCREEN S E.
TABASKA J E.
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                         21-APR-2005
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        ADX33652;
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(ZHOU/)
(KOVA/)
(SCRE/)
(TABA/)
(CAOY/)
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New recombinant DNA construct, useful for improving plant tolerance to oold, hear, drought, herbicides, extreme osmotic conditions, pathogens or pests, for confering increased resistance to plant disease, or for improving yield.

Claim 1; SEQ ID NO 16472; 15pp; English.

The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at available in electronic form from the US patent office at the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, increased resistance to plant disease, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert of the interest o nvention

Sequence 821 BP; 187 A; 227 C; 214 G; 193 T; 0 U; 0 Other;

ö 7.5%; Score 62; DB 13; Length 821; 00.0%; Pred. No. 6.9e-09; Indels 100.0%; Pred. nv. Query Match Best Local Similarity 100.0 Matches 62; Conservative

Gape

9 762 CAACTGAAAACAGCCGAGCGATCTCCTCCCTCTCCCTCTCCGATCCATTCTCCAGCGC 

AG 823

822 6

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Plant full length insert polynucleotide segid 32541. ADX61698 standard; cDNA; 1696 BP Kovalic DK, 28-APR-2003; 2003US-00425114 05-NOV-2001; 2001US-00985678 99US-00304517 (first entry) KOVALIC D K. SCREEN S E. TABASKA J E. CAO Y. WPI; 2004-180133/17. US2004034888-A1. Zhou Y, ZHOU Y. LIU J. 06-MAY-1999; Unidentified 21-APR-2005 19-FEB-2004. ADX61698; ring/) CAOY/) SCRE/) TABA/ Liu J, RESULT 15 ADX61698 

New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield; protein content; gene; ss. Tabaska JE, Screen SE, improving yield The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at the polynucleotide ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmocia conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle'pathway, for conferring increased resistance to plant disease, for producing galactomannan, lighth or plant growth regulators, for increasing the rate of homologous

Claim 1; SEQ ID NO 32541; 15pp; English.

or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert polynucleotide that can be used in the recombinant DNA construct of the

invention

recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake

ö 317 TGAATGGTTATTTTGCTTCAGATTAAAGCTAATTATTTAGACTGATGCAGCTGCAATTCAT 376 702 raagraecrerreecriteeaarraaaeceaecrerrieeaereereeaecrerarar 761 Gaps ō Length 1696; Sequence 1696 BP; 440 A; 429 C; 386 G; 441 T; 0 U; 0 Other; 20; Indels Score 60; DB 13; Pred. No. 4.6e-08; 0; Mismatches 20; 408 762 AGAGACAAAACATTGTAGAAACAGTAGAAGC 793 377 AGAGACAAAAACAGTGTAGAAGCCGTATAAGC 7.3%; ilarity 78.3%; Conservative Local Similarity ses 72; Conserv Query Match Matches S 셤 ò 셤 ð

Search completed: March 5, 2006, 13:39:26 Job time : 622 8ecs

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c         19         213.6         26.0         189962         14         AC147516         AC147616         AC147616         AC147616         AC147616         AC147617         <	DNA linear P phyta, Embryophyta, lopsida, Poales; Poa and Masucci,J.D. lective control of g	Plant regulacory sequences for selective control of gene Patent: WO 0183790-A 90 08-NOV-2001; Monsanto Technology LLC (US) Location/Qualifiers 1
GenCore version 5.1.7  Copyright (c) 1993 - 2006 Biocceleration Ltd.  OM nucleic - nucleic search, using sw model  Run on: March 5, 2006, 09:51:22 ; Search time 4261 Seconds  (without alignments)  10979.151 Million cell updates/sec  Title:  US-10-660-208-90  Perfect score: 823  Sequence: 1 ctgcacggtactccaagtatcgatccattctccagcgcag 823  Scoring table: IDENTITY_NUC  Gapop 10.0 , Gapext 1.0  Searched: 5883141 seqs, 28421725653 residues  Total number of hits satisfying chosen parameters: 11766282  Minimum DB seq length: 0  Maximum DB seq length: 2000000000  Post-processing: Minimum Match 100*  Listing first 45 summaries		the number eater than or exercitly eater than or exercitly eater than or exercitly eater than or exercitly eater than or exercitly eater than or exercitly eater than or exercitly eater than or exercitly eater than eater

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Zea mays strain B73 clone ZWMBBb0160F12, *** SEQUENCING IN PROGRESS ***, 13 unordered pieces.
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae, PACCAD clade, Panicoldeae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (15-JAN-2005) The Institute for Genomic Research (TIGR) 9712 Medical Center Dr. Rockville, MD 20850 at base 1 to 149882) Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H., Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H., Utterback, T.R., Peldblyum, T.V., Rabinowicz, P., Fraser, C.M., Schubert, K., Sanhiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T., Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and Quackenbush, J.
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                                                                                                                           TIGCIGAAATTATAGCGAGGGCCCAACGCCCATCACTTCGAGGTCAGCATGTAC
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Plant regulatory sequences for selective control of gene expression
Patent: WO 0183790-A 87 08-NOV-2001;
Monsanto Technology LLC (US)
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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                                                                      661 GCCGCAGTGAGGCCAAGCCGGCCGGTCGTCGTCCACCACCACCCCCCCTTTTATACTAT
                                                    TACAGTTGTTGCAACGTGAATGGTTATTTGCTTCAGATTAAAGCTAATTATTTAGACTGA
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Pred. No. 2e-146;
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AX299946
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/db_xref="taxon:4577"
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/organism="Zea mays"
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Similarity 99.1%;
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FEATURES

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Zea mays strain B73 clone ZWWBBC0261N01, *** SEQUENCING IN PROGRESS ***, 31 unordered pieces.
                                                                                                                                                                                                                                                        181 CTGCACGGTACTCCAAGTATAAGACACAGCTAAAACACATAATACAGTGGTCATGTC 51122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (25-JAN-2005) The Institute for Genomic Research (TIGR), 9712 Medical Center Dr. Rockville, MD 20850 On Jan 25, 2005 this sequence version replaced gi:57863129.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
1 (bases 1 to 182004)
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Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H.,
Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H.,
Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M.,
Schubert, K., Sanwiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T.,
Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chan, A.P., Perrea, G., Zheng, L., Cheung, P., Lee, D., Koo, H., Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M., Schubert, K., Sanwiguel, P., Ma, J., Pontaroli, A.C., Roblfing, T., Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and Quackenbush, J.
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                                                                                                                                                                                                                                                                                             61 TAAAACATGTGTCTTACCATATTCATTGTATCAATCAGAACATTCAATAAATTAAAGTGA
                                                                                                                                                                                                                   CTGCACGGTACTCCAAGTATAAGACACAGGTAAAACACAACATAATGCAGTGGTCATGTC
                                                                                                                                                                              Gape
                                                                                                                                    Length 149882;
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                                                                                                                                                                           Indele
                                                                                                                                  Score 252; DB 14;
Pred. No. 4.2e-59;
0; Mismatches 5;
  /estimated_length=unknown
143473. .143572
                                   /estimated length=unknown 147243. .147342
                                                                              estimated_length=unknown
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HTG; HTGS_PHASE1.
Zea mays
                                                                                                                                      Query Match
Best Local Similarity 98.1%;
Matches 255; Conservative
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KEYWORDS
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                                                                            for Genomic Research (TIGR),
Schubert, K., Sanwiguel, P., Ma, J., Pontaroli, A.C.; Rohlfing, T., Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and Quackenbush, J.
                                                 Direct Submission
Submitted (25-JAN-2005) The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850
On Jan 25, 2005 this sequence version replaced gi:57862916.
                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                contig of 2769 bp in length gap of unknown length contig of 2051 bp in length gap of unknown length contig of 44743 bp in length gap of unknown length gap of unknown length contig of 33189 bp in length contig of Marown length gap of unknown length contig of 4674 bp in length gap of unknown length contig of 4674 bp in length gap of unknown length
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contig of 16341 bp in length
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gap of unknown length
contig of 8136 bp in length
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contig of 3670 bp in length
gap of unknown length
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unknown length
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Location/Qualifiers
                                                                                                                                                                                              Web site: http://www.tigr.org/tdb/tgi/maize/
Contact: maize@tigr.org
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/estimated length=unknown
68664. 68763
/estimated length=unknown
101953. 102052
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/estimated length=unknown
112742. .112841
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2770. .2869
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Seq lib_id: ZOCR
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Score 251.8; DB 14; Length 182004; Pred. No. 4.8e-59;
4 178763: gap of unknown length
4 182004: contig of 3241 bp in length.
Location/Qualifiers
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40513. 40512
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                                                                                                                                                                                                                                                                                                                                                   /8862. .43961
/estimated length-unknown
48430. .48529
/estimated length-unknown
59230. .59329
/estimated length-unknown
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                                                                                                                                                                                                                                                                                    estimated length=unknown 2649. 32748
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estimated length-unknown
15148. .65247
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5494. .85593
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1577. .21676
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                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 31 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as soon as it is available and the accession number will be preserved.
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nknown length
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of 16617 bp in length
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of 20883 bp in length
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                            Web site: http://www.tigr.org/tdb/tgi/maize/
Contact: maize@tigr.org
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    Center name: TIGR
Seq_lib_id: ZGGT
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Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H., Utterback, T.R., Peldblyum, T.V., Rabinowicz, P., Fraeer, C.M., Schubert, K., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T., Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and Quackenbush, J. Chan, A.P., Edell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and Consortium for Maize Genomics - BAC skim sequencing and assembly Unpublished  2. (bases 1 to 193326) Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H., Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraeer, C.M., Schubert, K., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T., Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and Char, Center Dr., Rockville, MD 20850 3. (bases 1 to 193326) Chan, A.P., Portea, G., Zheng, L., Cheung, P., Lee, D., Koo, H., Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraeer, C.M., Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraeer, C.M., Barbazuk, B., Bennetzen, J. and Maidman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and	Ouackenbush.J.  Direct Submission  Submitted (25-JAN-2005) The Institute for Genomic Research (TIGR),  9712 Medical Center Dr. Rockville, MD 20850  On Jan 25, 2005 this sequence version replaced gi:57863099.  Center name: TIGR  Seq_115_id: ZGS	1946: contig of 5678 18531: contig of unknown 18531: contig of unknown 23105: contig of unknown 31291: contig of unknown 31291: contig of 874 23105: gap of unknown 40475: contig of 9184 40575: gap of unknown 55208: contig of 4765 56239: contig of 4799 56239: contig of 4799 56590: contig of 4799 55808: gap of unknown 55708: contig of 1786 66590: contig of 1787 74475: contig of 1788 66580: contig of 1787 74575: gap of unknown 84289: contig of 1788 86286: contig of 2627 86686: contig of 2637 86786: gap of unknown 89393: contig of 2671 89495: gap of unknown 89393: contig of 2671 89495: gap of unknown 89393: contig of 2671 89495: gap of unknown 104790: contig of 5295
CTGCACGGTACTCCAAGTATAAGACACAACATAATGCAGTGCTATGTC 60	TITLE JOURNAL AY664417 Sequence split into 4 fragments LOCUS AY664417 Accession AY664417 Sequence split into 4 fragments LOCUS AY664417 Accession AY664417 Sequence split into 4 fragments LOCUS AY664417 Accession AY664417 AY664417 1 10001 210000 AY664417 2 20001 310000 AY664417 3 30001 310000 AY664417 3 20001 310000 AY664417 1 10001 300001 310000 AY664417 2 20001 310000 AY664417 3 30001 310000 AY664417 2 20001 310000 AY664417 3 30001 310000 AY664417 2 20001 310000 AY664417 2 20001 310000 AY664417 3 30001 310000 AY664417 2 20001 310000 AY664417 2 20001 310000 AY664417 2 30001 310000 AY664417 2 30001 310000 AY664417 3 30001 3	Db 88571 TANAGATGGTCTTACCATATCATTACTATCATACAATCAGGCATTCAATAAATTAAAGTGA 88512  Oy 121 CCAATCAGATAGTCTCTGTCCGAATATCATTCATTGTACCAATCAGGCATTCAATAAATTAAAGTGA 88512  Db 88511 CCAATCAGATAGTCTTCTGTCTCGAATATAGAACTGGTCTTCATCAGATA 180

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contig of 13541 bp in length.
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contig of 2277 bp in length
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/organism="Zea mays"
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/strain="B73"
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clone="ZMMBBc0190D10"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAAAACATGTGTGTTTAACCATATTCATTGTATCAATCAGAACATTCAATAAATTAAAGTGA 120
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29.5%; Score 242.6; DB 14; Length 193326;
Best Local Similarity 94.7%; Pred. No. 1.8e-56;
Matches 251; Conservative 0; Mismatches 14; Indels 0; G
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51366. .151465
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73402. .173501
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Zea mays Zea mays Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,

AC155517.2 GI:58082377 HTG; HTGS\_PHASE1.

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145856 CCAATCAGCTAGCCTCCTGTCTCGAACATAGAGCTAAGACACTGTGTGTCTTCGTCAAGATA 145797
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Zea mays clone ZMMBBc0496L17, *** SEQUENCING IN PROGRESS ***, 2
ordered pieces.
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Zea mays
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
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HTG; HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN.
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                                         organism="Zea mays"
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Matches 249; Conservative
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Submitted (15-JAM-2005) The Institute for Genomic Research (TIGR),
9712 Medical Center Dr, Rockville, MD 20850
3 (bases 1 to 148120)
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
                                         Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H., Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M., Schubert, K., Sanmiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T., Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and Quackenbush, J.
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                                                                                                                                                                                           2 (bases 1 to 148120)
Chan,A.P., Pertea,G., Zheng,L., Cheung,F., Lee,D., Koo,H.,
Utterback,T.R., Feldblyum,T.V., Rabinowicz,P., Fraser,C.M.,
Schubert,K., SanMiguel,P., Ma,J., Pontaroli,A.C., Rohlfing,T.,
Budinan,A., Bedell,J.A., Lakey,N., Barbazuk,B., Bennetzen,J. and
Quackenbush,J.
                                                                                                                                                      Consortium for Maize Genomics - BAC skim sequencing and assembly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (25-JAN-2005) The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850
On Jan 25, 2005 this sequence version replaced gi:57863038.
--------Trace submission
Center_name: TIGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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9 of 30354 bp in length
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Web site: http://www.tigr.org/tdb/tgi/maize/
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Birren, B., Nusbaum, C., Lander, E., Butler, E., Wing, R., Bharti, A.K., Messing, J., Abouelleil, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pherre, M., Hafez, M., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, G., Liu, A., Mabbltt, R., Machean, C., Macdonald, P., Marier, J., Mathews, C., McCarthy, M., Meldrim, J., Mapor, T., Micol, R., Norbu, C., O'Connor, T., O'Donnell, P., Nayen, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., Radunga, L., Mihova, T., Retra, R., Kase, C., Rogov, P., Ramsan, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramsang, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Sewery, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Vassiliev, H., Venkataraman, V., Zembek, L., Zimmer, A. and Zody, M. Buhritted, (night) Breez, Bunkishon, Brenz, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Brenz, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Armer, Arm
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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On Jan 14, 2005 this sequence version replaced gi:49035067.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
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Contact: sequence_submissions@broad.mit.edu
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Bharti, AK and Messing, J: The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers, The State University of New Jersey, 190 Frelinghuysen Road, Piscataway, NJ 08854, USA (http://pgir.rutgers.ed) Buller, E and Wing, R: Arizona Genomics Institute, Biological Sciences West, 448A, P.O. Box 210088, University of Arizona,

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I43793 bp DNA linear HTG 03-FEB-2005 Zea mays clone ZMMBBC0051H21, *** SEQUENCING IN PROGRESS ***, 8
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1 (bases 1 to 143793)

Birren, B., Nusbaum, C., Lander, E., Butler, E., Wing, R., Bharti, A.K. and Messing, J.
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                                                                                              * NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. Gaps between the contigs are presented as tune of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* the accession number will be preserved.

* 62678 contig of 62677 bp in length 62677 contig of 62677 bp in length.

* 62678 li2468; contig of 49691 bp in length.

* 1. 112468

| Organism="Zeomismo" contig of 49691 bp in length.
| Organism="Zeomismo" contig of 49691 bp in length.
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AC149827.2 GI:57790148
HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
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/db xref="taxon:4577"
/clone="ZMMBBc0496L17"
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Best Local Similarity 94.2%;
Matches 245; Conservative (
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Direct Submission

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Research, 320 Charles Street, Cambridge, MA 02141, USA

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Sarachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boucher, C., Cooke, P., Conum, B., DeArellano, K., Diaz, J.S., Dodge, S., FitzGerald, M., Gage, D., Galagan, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Hagopian, D., Hagopian, L., Grand, P., Hall, J., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatea, A., Kalls, C., Landers, T., Levine, R., Lindblad - Toh, K., Liu, G., Liu, G., Liu, A., Mabblatt, R., Maclean, C., Macdonald, P., Major, J., Manning, J., Mathews, C., McCarthy, M., Meldrim, J., Nicol, R., Norbu, C., O'Connor T., O'Donnor T., O'Donnor I., Nicol, R., Norbu, C., O'Connor T., O'Donnor I., Ramaeamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schubeack, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Vassillev, H., Vonkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Suphission
Messing, J., Abouelleil, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H.M., Barra, N., Bastien, V., Bloom, T., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymoxe, A., Cook, A., Cooke, P., Carum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Gardon, S., Ferreiza, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., FitzGerald, M., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Jones, C., Mantine, W., Mathews, C., Maccan, C., Macdonald, P., Marier, J., Manning, J., Mathews, C., McCarthy, M., Meldrim, J., Manning, J., Mathews, C., McCarthy, M., Meldrim, J., Manning, J., Mathews, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Stojanovic, N., Stubbs, M., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Travers, M., Vassiliev, H., Venkataraman, V., Zembek, L., Zimmer, A. and Zody, M. Direr, Subrission
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Butler, E and Wing, R: Arizona Genomics Institute, Biological Sciences West, 448A, P.O. Box 210088, University of Arizona, Tucson, AZ 85721, USA (http://www.genome.arizona.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (03-FEB-2005) Broad Institute of MIT and Harvard, 320 Charles Street, Cambridge, MA 02141, USA On Jan 14, 2005 this sequence version replaced gi:49035053.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Contact: sequence_submissions@broad.mit.edu
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29099 TAAAAACGTGTGTCTTACCATATTCATTGTACCAATCAGAACATTTAATAAATTAAAGTGA 29040
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Zea mays inbred B77 beta-keto acyl reductase gene, partial cde.
AF348367.1 GI:19070512
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runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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28.7%; Score 236; DB 14; Length 143793;
Best Local Similarity 94.2%; Pred. No. 1.3e-54;
Matches 245; Conservative 0; Mismatches 15; Indels 0;
                                                                                     contig of 30907 bp in length gap of unknown length contig of 5266 bp in length contig of 5266 bp in length contig of 9209 bp in length gap of unknown length contig of 3209 bp in length gap of unknown length gap of unknown length contig of 21172 bp in length contig of 11172 bp in length gap of unknown length contig of 11172 bp in length contig of 11172 bp in length
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21040: gap of unknown length
23150: contig of 2110 bp in length
23250: gap of unknown length
43793: contig of 20543 bp in length.
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'db_xref="taxon:4577"
'clone="ZMMBBC0051H21"
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2 (bases 1 to 117844)
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                     Spermatophyta, viildiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 1257)
Dietrich, C.R., Cull, F., Packila, M.L., Li, J., Ashlock, D.A.,
Nikolau, B.J. and Schmable, P.S.
Maize Mu transposons are targeted to the 5' untranslated region of the 918 gene and sequences flanking Mu target-site duplications exhibit nonrandom nucleotide composition throughout the genome Genetics 160 (2), 697-716 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="AALB3B98.1"
/db_xref="G1:19070513"
/translation="MAGTCAHVEFLRAQPAWALALAAVGLLVAVRAARFALWVYAAF
LRPGKPLRRRYGAWAVVTGATDGIGRAVAFRLAASGLGLVLVGRNQEKLAAVAAEIKA
RH"
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*** SEQUENCING IN PROGRESS
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                                                                                                                                                                                             Dietrich, C.R., Packila, M.L., Li, J., Ashlock, D.A., Nikolau, B.J. and Schnable, P.S.
Direct Submission
Submitted (12-FBB-2001) Zoology and Genetics, Iowa State University, B420 Agronomy Hall, Ames, IA 50011, USA
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28.6%; Score 235.2; DB 15; Length 1257; 93.2%; Pred. No. 1.9e-54;
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0
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Zea mays strain B73 clone ZMMBBb0026K01,
***, 17 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                               /organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="inbred B77"
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                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:4577"
<946. .>1257
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HTG; HTGS_PHASE1.
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta, Lillopsida, Poales, Poaceae, PACCAD
clade, Panicoldeae, Andropogoneae, Zea.
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Submitted (15-JAN-2005) The Institute for Genomic Research (TIGR),
9712 Medical Center Dr. Rockville, MD 20850
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                                                                                                                                                        Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H., Leterback, T.R., Peldblyum, T.V., Rabinowicz, P., Fraser, C.M., Schubert, K., Sanwiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T., Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and Quackenbush, J.
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Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H.,
Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H.,
Chubert, K., Sanwiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T.,
Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and
Quackenbush, J.
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12974: gap of unknown length
15100: contig of 2136 bp in length
1510: gap of unknown length
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of 3456 bp in length
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1 110623: contig of 8313 bp in length
4 110723: gap of unknown length
4 114040: contig of 3317 bp in length
1 114140: gap of unknown length
1 117844: contig of 3704 bp in length.
Location/Qualifiers
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/estimated_length=unknown
39874. 39973
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RESULT 12 AC155367

linear HTG 25-JAN-2005 Direct Submission Submitted (15-JAN-2005) The Institute for Genomic Research (TIGR), 9712 Medical Center Dr, Rockville, MD 20850 Submitted (25-JAN-2005) The Institute for Genomic Research (TIGR), 9712 Medical Center Dr. Rockville, MD 20850 On Jan 25, 2005 this sequence version replaced gi:57862888. Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; PACCAD clade; Panicoldeae; Andropogoneae; Zea. 1 (bases 1 to 1703) (Chan, A.P., Pectan, A.P., Cheung, F., Lee, D., Koo, H., Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M., Schubert, K., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T., Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and Quackenbush, J. Chan, A.P., Perten, G., Zheng, L., Cheung, F., Lee, D., Koo, H., Utterback, T.R., Peldblyum, T.V., Rabinowicz, P., Fraser, C.M., Schubert, K., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T., Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and Quackenbush, J. Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H., Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M., Schubert, K., Sanwiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T., Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and Quackenbush, J. Consortium for Maize Genomics - BAC skim sequencing and assembly NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. f unknown length g of 2461 bp in length f unknown length g of 3068 bp in length f unknown length length bp in length length bp in length contig of 3163 bp in length gap of unknown length contig of 2199 bp in length gap of unknown length length bp in length length bp in length of 3288 bp in length bp in length Web site: http://www.tigr.org/tdb/tgi/maize/ length unknown contig gap of gap of 23289 23389 26300 26400 28051

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241	1773	gap
99316	458	gap
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QY 121 CCAATCAGATAGTCTCTGTCCCGA	74033300. /estimated_length=unknown	gap
Db 99196 TAAAACATGTGTCTTACGATATTTA	68t;	14 C 15 m 10 C
Oy 61 TAAAACAIGIGICIIACCAIAIICA	/clone="ZWMBBb0092I04"	Ç
95156	Btra B	
1 6	nism="Zea mays type="genomic	
. THECACGETACTCCAAGTATAAGAC	1170318	8
Best Local Similarity 93.8%; Pred. Matches 244; Conservative 0; Mi	126	2007
	150462 150561: gap of unknown 150562 158664: contig of 8103	
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/estimated_le	545 136644: gap or un 645 146242: contig.of	
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gap 124316 .12415'	119700 119799: GONLLIG OL 2130	
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gap 1197001 <u>1</u> 9799 /estimated lengths	114448: GONCLES OF UNKNOWN	
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rity 93.8%; Pred. No. 3.5e-54;
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PLN 09-MAY-1996

linear

DNA

6343 bp

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Unpublished
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KEYWORDS
SOURCE
ORGANISM
                                                                        DEFINITION
                   RESULT 14
AC151050
LOCUS
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                                                                                   Tacke, E., Korfhage, C., Michel, D., Maddaloni, M., Motto, M.,
Lanzini, S., Salamini, F. and Doring, H.P.
Transposon, tagging of the maize Glossy2 locus with the transposable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NDCGVRIVEARCDRDMAEWIRDAAPGRIRQLCYDKVLGPELFFSPLLYVQITNFKCGG
LALGFSWAHLIGDIPSAATCFNKWAQILSGKKPEATVLTPPNQPLQGQSPAAPRSVKQ
VGPIEDLWLVPAGRDMACYSFHVSDAVLKKLHQQQNGRQDAAAGTFELVSALVWQAVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KIRGDVDTVTVVRADAAGRSGKSLANEMKVGYVESAGSSPAKTDLAELAALLAKNLVD
ETAAVAAFQGDVLVYGGANLTLVDMEQVDLYGLEIKGQRPVHVEYGMDGVGDEGAVLV
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                                                                                                                                                                                                                               Direct Submission
Submitted (19-JUN-1995) E. Tacke, Max-Planck-Institute, Dept.
Salamini, Carl-von-Linne-Weg 10, 50829 Koeln, NRW, FRG
Location/Qualifiers
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Pred. No. 3.9e-52;
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HTG; HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN.
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121770. 121869
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                                                                                                                                                  Bharti, AK and Messing, J: The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers, The State University of New Jersey, 190 Freilinghuysen Road, Piscataway, NJ 08854, USA (http://pgir.rutgers.edu)
Butler, E and Wing, R: Arizona Genomics Institute, Biological Sciences West, 448A, P.O. Box 210088, University of Arizona, Tucson, AZ 85721, USA (http://www.genome.arizona.edu)
Center project Indomes: L30292
Center project name: L30292
Center clone name: 243_P_6
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
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gap of unknown length
gap of unknown length
contig of 18812 bp in length
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gap of unknown length
contig of 5444 bp in length
gap of unknown length
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of 4026 bp in length
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                                                                                      Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@broad.mit.edu
            Center: Broad Institute of MIT and Harvard Center code: WIBR
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sequence as soon as it is available and

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Rise, C., Rogov, P., Severy, P., Smith, C.

n number will be preserved.
20266: contig of 20266 bp in length
20366: gap of 100 bp
78734: gap of 100 bp
40318: contig of 61584 bp in length

20267 20367 78635 78735

us-10-660-208-90.rge

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Vassiliev, H. Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission Submitted (01-JUL-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA (bases 1 to 198102) TITLE JOURNAL

Submitted (202-70M-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 16, 2004 this sequence version replaced gi:48717652. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997). http://ftp.genome.washington.edu/RM/RepeatMasker.html

COMMENT

------ Genome Center Center: Whitehead Institute/MIT Center for Genome Research Web site: http://www-seq.wi.mit.edu Contact: sequence\_submissions@broad.mit.edu code: WIBR

Bharti, AK and Messing, J: The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers, The State University of New Jersey, 190 Frelinghuysen Road, Piscataway, NJ 08854, USA (http://pgir.rutgers.edu)
Butler, E and Wing, R: Arizona Genomics Institute, Biological Sciences West, 448A, P.O. Box 210088, University of Arizona, Tucson, AS 5721, USA (http://www.genome.arizona.edu)

Center project name: L29613

Center clone name: 54 A 1

Center clone name: 54 A 1

This consensus information

This consensus is derived from a shotgun assembly that has been manually curated. It is the best representation of the BAC that we can generate without further laboratory work. The draft assembly has been edited, and if possible, ends identified by vector as well as by BAC end sequences, and contigs ordered and oriented. Bases that are not Ns are either above Q20 or manually edited. This assembly was performed with phrap. All trace files for this project are available at the NCBI trace repository

(http://www.ncbi.nlm.nh.gov/Traces/trace.fcgi?). An exact list of reads used in this assembly are available at http://www.broad.mit.edu/annotation/plants/maize/randomclones.html:

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173658 GIGTCTTGAGTTTTTTTACATTCACCCCCTAGACACGCTGTAAGACACAACTTAAAACA 173717
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20267._.20366
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91.2%; Pred. No. 4.8e-51;
ive 0; Mismatches 23; Indels
140418: gap of 100 bp
198102: contig of 57684 bp in length.
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|mol type="genomic DNA"
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Job time : 4265 secs
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Matches 248; Conservative
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NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces

is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

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Sequence 87, App
Sequence 13667,
Sequence 13680,
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Sequence 13673,
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Sequence 16647,
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1: /cgr12 6/prodata1/pubpna/USO1 PUBCOMB.seq:*
2: /cgr12 6/prodata1/pubpna/USO1 PUBCOMB.seq:*
2: /cgr12 6/prodata1/pubpna/USO9A PUBCOMB.seq:*
4: /cgr12 6/prodata1/pubpna/USO9B PUBCOMB.seq:*
5: /cgr12 6/prodata1/pubpna/USO9B PUBCOMB.seq:*
6: /cgr12 6/prodata1/pubpna/USO9B PUBCOMB.seq:*
7: /cgr12 6/prodata1/pubpna/USO9B PUBCOMB.seq:*
8: /cgr12 6/prodata1/pubpna/USOPUBCOMB.seq:*
9: /cgr12 6/prodata1/pubpna/USOPUBCOMB.seq:*
10: /cgr12 6/prodata1/pubpna/USOPUBCOMB.seq:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                                                                                 nucleic search, using sw model
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Maximum DB seq length: 2000000000
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	Sequence 3355, Ap	GENERAL INFORMA	Sequence 15, Appl	Sequence 16, Appl	Sequence 8, Appli	Sequence 27876, A	Sequence 36797, A	Sequence 145839,	Sequence 118219,	Sequence 78019, A	Sequence 64, Appl		5114			Sequence 130682,	Seguence 171134,	26114,	Sequence 35755, A	Sequence 66476, A	477,	Sequence 22, Appl	
	US-10-425-115-3355	US-10-759-602-1	US-10-759-602-15	US-10-759-602-16	US-09-950-933A-8	US-10-425-114-27876	US-10-425-115-36797	US-10-425-115-145839	US-10-425-115-118219	US-10-425-115-78019	US-09-846-903-64	US-10-660-208-64	US-10-437-963-51148	US-10-739-930-2967	US-10-425-115-10426	US-10-425-115-130682	US-10-425-115-171134	US-10-767-701-26114	US-09-925-065A-35755	US-09-925-065A-66476	US-09-925-065A-66477	US-10-322-696-22	
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                                                     GENERAL INFORMATION:
APPLICANT: Conner, Timothy W.
APPLICANT: Dubois, Partice
APPLICANT: Dubois, Partice
APPLICANT: Malven, Marianne
APPLICANT: Masucci, James D.
TITLE OF INVENTION: PLANT REGULATORY SEQUENCES FOR SELECTIVE CONTROL
TITLE OF INVENTION: OF GENE EXPRESSION
FILE REFERENCE: 38-21(15678) B promoters
CURRENT FILING DATE: 2001-04-26
PRIOR PLLING DATE: 2001-04-26
PRIOR PLLING DATE: 2001-04-26
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 CCAATCAGATAGTCTCCCTGTCCCGAATATAGAGCTAAGACACTGTGTCTTCGTCAAGATA
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100.0%; Score 823; D
Best Local Similarity 100.0%; Pred. No. 0;
Matches 823; Conservative 0; Mismatches
Sequence 90, Application US/09846903
Publication No. US20030200565A1
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ORGANISM: Zea mays
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Fublication No. US20030200565A1

GENERAL INFORMATION:

APPLICANT: Conner, Timothy W.

APPLICANT: Malven, Marianne

APPLICANT: Malven, Marianne

APPLICANT: Malven, Marianne

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APPLICANT: Malven, Marianne

APPLICANT: Malven, Marianne

TITLE OF INVENTION: OF GENE EXPRESSION

TITLE OF INVENTION: OF GENE EXPRESSION

TITLE OF INVENTION NUMBER: US 60/201,255

PRIOR PRIOR PELLING DATE: 2000-05-01

NUMBER OF SEQ ID NOS: 98

SOOTWARE: PatentIn Ver. 2.1
                                                                                                                                     CCAATCAGATAGTCTCCTGTCCCGAATATAGAGCTAAGACACTGTGTCTTCGTCAAGATA
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ORGANISM: Zea mays
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LENGTH: 1587
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100.0%; Score 823; D
Best Local Similarity 100.0%; Pred. No. 0;
Matches 823; Conservative 0; Mismatches
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; Sequence 90, Application US/10660208
; Publication No. US20040133946A1
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; ORGANISM: Zea mays
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Sequence 1367, Application US/10425115
Sequence 13667, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Stou, Yihus
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21(5322)B
CURRENT FILLING DATE: 2003-04-28
CURRENT FILLING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 13667
LENGTH: 875
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Sequence 13680, Application US/10425115
Sequence 13680, Application WS/10425115
Sequence 13680, Application WS/10425115
SEMERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovallc, David K.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
1151 TAAGCAAACAAGCGAACATTGCTTAGCTACAACCAATTTGCTGGGCTTCCATGGGCATCG 1210
                                                                                                                                                                                           1271 ACTTCGAGGTCAGCATTGTACTTTTGTTAACGTCTCGATAAATTTGTTCACTTAAAATAG 1330
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                                             471 CAGAAGTATTGTGGCTGCATATTGCTGAAATTATAGCGAGGGCCCAAGGCCCATCACTTC
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100.0%; Pred. No. 2.6e-30;
tive 0; Mismatches 0;
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US-10-425-115-13667
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Best Local Similarity 100.
Matches 75; Conservative
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APPLICANT: Malven, Marianne
APPLICANT: Malven, Marianne
APPLICANT: Malven, Marianne
APPLICANT: Malven, Marianne
APPLICANT: Malven, Marianne
TITLE OF INVENTION: PLANT REQUENCES FOR SELECTIVE CONTROL
TITLE OF INVENTION: OF GENE EXPRESSION
FILE REFERENCE: 38-21(15678) B promoters
CURRENT APPLICATION NUMBER: US/10/660,208
CURRENT FILING DATE: 2003-09-11
PRIOR PLICATION NUMBER: US 60/201,255
PRIOR FILING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 98
SOFTWARE PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                        CAGAAGTATTGTGGCTGCATATTGCTGAAATTATAGCGAGGGCCCAAGGCCCATCACTTC
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                                           Score 473; DB 3; Length 1587;
Pred. No. 3.6e-251;
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                           57.5%; Scor. 100.0%; Pred. No. ...
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Publication No. US20040133946A1
GENERAL INFORMATION:
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                                                                                           Conservative
                                                                    Similarity
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; ORGANISM: Zea mays
US-10-660-208-87
                                                                    Best Local Simi
Matches 473;
US-09-846-903-87
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                                           Query Match
Best Local (
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 13677
LENGTH: 894
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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
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                                                                                                                                                                                                                                                                                                                                                                                                   758 GAAGCAACTGAAAACAGCCGAGCGATCTCCTCTCCCTCTCC
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Best Local Similarity 100.0%; Pred. No. 2.5e-25;
Matches 66; Conservative 0; Mismatches 0;
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US-10-425-115-13677
                                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: MRT4577_112460C.1 US-10-425-115-13673
             CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 13673
LENGTH: 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13677, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
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Publication No. US20040034888A1
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                                                                                                                                             TYPE: DNA ORGANISM: Zea mays FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Zea mays
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Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: ADOU, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21(5322) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
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8.9%; Score 73; DB 8; L
Best Local Similarity 100.0%; Pred. No. 3.3e-29;
Matches 73; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                        , OTHER INFORMATION: Clone ID: MRT4577_112467C.1
US-10-425-115-13680
TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 13680
LENGTH: 1251
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SEQ ID NO 13670
LENGTH: 859
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                                                                                                                                                                              TYPE: DNA ORGANISM: Zea mays FEATURE:
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APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molec
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molec
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molec
TITLE OF INVENTION: Plants and Uses Thereof for Plant Imps
CURRENT PAPLICATION NUMBER: US/10/425,114
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 12914
TYPE
TYPE
TYPE
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US-10-425-114-12914
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100.0%; Pred. No. 1.9e-21;
                                                                                                                                                                                                                                                                                                                               Score 62; DB 7; I
Pred. No. 4.2e-23;
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COTHER INFORMATION: Clone ID: LIB3066-004-E5_FLIUS-10-425-114-16472
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TITLE OF INVENTION: Nucleic Acid Molecules an TITLE OF INVENTION: Plants and Uses Thereof PILE REFERENCE: 38-21(53313)8
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 16472
LENGTH: 821
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7.5%; Score 62; DB
Best Local Similarity 100.0%; Pred. No. 4.2
Matches 62; Conservative 0; Mismatches
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Publication No. US20040034888A1
GENERAL INFORMATION:
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Publication No. US20040034888A1
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APPLICANT: Zhou, Yihuu
APPLICANT: Kovalic, David K:
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
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Best Local Similarity 100.
Matches 59; Conservative
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ORGANISM: Zea mays
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ORGANISM: Zea mays
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Chou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REPERENCE: 38-215322) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
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                                                                                                                                                                                                                                                                                                                                                       Gaps
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  TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21 (53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
LENGTH: 485
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100.0%; Pred. No. 1.2e-23;
iive 0; Mismatches 0;
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US-10-425-114-23949
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US-10-425-115-134827
                                                                                                                                                                                                                                                                                                       7.7%; Score 63; DB 100.0%; Pred. No. 1.1 itive 0; Mismatches
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Publication No. US20040034888A1
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Kovalic, David K
                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.C
Matches 63; Conservative
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Best Local Similarity 100.
Matches 63; Conservative
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APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David
APPLICANT: Screen, Steven
APPLICANT: Tabaska, Jack
APPLICANT: Tabaska, Jack
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                                                                                                                                                                                                                                                                                                                                                                                                   183 TGTCTTGAGAT1
                                                                                                                                                            TYPE: DNA
ORGANISM: Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA .
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243 CCA 245
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Sequence 39694, Application US/10425115
Sequence 39694, Application US/10425115
Fublication No. US20040214272A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Con, Yongue
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
CURRENT APPLICATION NUMBER: 108/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 39694
LENGTH: 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTCCAGCGCAG 823
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                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53313)B CURRENT APPLICATION NUMBER: US/10/425,114 CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 73128 SEQ ID NO 12891 LENGTH: 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                        Query Match 7.2%; Score 59; DB 7; Length 795; Best Local Similarity 100.0%; Pred. No. 1.9e-21; Matches 59; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 6.0%; Score 49; DB 8; Length 178; Best Local Similarity 100.0%; Pred. No. 6.2e-16; Matches 49; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                              TYPE: DNA
ORGANISM: Zea mays
FRATURE:
OTHER INFORMATION: Clone ID: CC-ZMF0148038E03_FLI
US-10-425-114-12891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: MRT4577_136201C.1 US-10-425-115-39694
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NAME/KEY: unsure
LOCATION: (1)..(178)
FEATURE INFORMATION: unsure at all n locations
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      765 CTGAAACAGCCGAGCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Zea mays
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Search completed: March 5, 2006, 11:39:06 Job time : 862 secs

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Sequence 66476, Application US/09925065A Publication No. U920040181048A1 GENERAL INFORMATION:
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US-09-925-065A-66476/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 35755
LENGTH: 1471
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Sequence 395, App
Sequence 1382480,
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Sequence 17868, A
                                                                                                                                           March 5, 2006, 11:26:37; Search time 509 Seconds (without alignments) 3545.020 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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| cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-11-124-367A-26026
US-09-92-065A-546671
US-10-330-773-772
US-10-330-773-937
US-10-995-561-13346
US-10-330-773-416
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Perfect score:
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. Sequence 24839, A	Sequence 25079, A	Seguence 4974, Ap	Sequence 917593,	Sequence 917594,		Sequence 327497,	Sequence 930919,	Sequence 746493,	Seguence 796124,	25441		Sequence 787721,	Sequence 168639,	Sequence 570511,	Sequence 20117, A			Sequence 939827,	939			Sequence 653866,	Sequence 732177,	Sequence 811564,
US-11-124-367A-24839	US-11-124-367A-25079	US-09-925-065A-4974	US-09-925-065A-917593	US-09-925-065A-917594	US-09-925-065A-141505	US-09-925-065A-327497	US-09-925-065A-930919	US-09-925-065A-746493	US-09-925-065A-796124	US-09-925-065A-254418	US-09-925-065A-254419	US-09-925-065A-787721	US-09-925-065A-168639	US-09-925-065A-570511	US-09-925-065A-20117	US-09-925-065A-141509	US-09-925-065A-21876	US-09-925-065A-939827	US-09-925-065A-939828	US-09-925-065A-413845	US-09-925-065A-793626	US-09-925-065A-653866	US-09-925-065A-732177	US-09-925-065A-811564
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19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	73	19
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
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100.0%; Pred. No. 0.15;
tive 0; Mismatches
                                     cation US/09925065A
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                                     Sequence 35755, Application US/
Publication No. US20040181048A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 22; Conservative
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US-09-925-065A-35755
US-09-925-065A-35755/c
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APPLICANT: "LANGE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONTINE CONT
Sequence 26025, Application US/11124367A Publication No. US20060024700A1 GENERAL INFORMATION:
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CORGANISM: Homo sapiens
US:11-124-367A-26025
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Best Local Similarity
Matches 21; Conserv
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE REPERBNCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR PILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2000-11-6
PRIOR PILING DATE: 2001-01-6
PRIOR PILING DATE: 2001-01-6
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PRIOR PILING DATE: 2001-01-7
PRIOR PILING DATE: 2001-01-7
PRIOR PILING DATE: 2001-01-7
PRIOR PILING DATE: 2001-01-7
         APPLICANT: Wang, David G.
ITILE OF INVENTION: Identification and Mapping of Single
ITILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
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Pred. No. 0.16;
                                                                                                                                                                       FILE KEFERENCE 100627.133
CURRENT PEPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR PILING DATE: 2001-024
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-30
PRIOR PELING DATE: 2000-11-30
PRIOR PELING DATE: 2000-11-30
PRIOR PELING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SEQ ID NO 66476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.7
Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                           ILE REFERENCE: 108827.135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-66476
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Best Local Similarity
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Gaps

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Indels

2.6%; scc. 100.0%; Pred. No. 0; Mismatches

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TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Genetic Polymorphisms Associated by
CURRENT PILICATION NUMBER: US/11/124,367A
CURRENT FILING DATE: 2005-05-09
PRIOR FILING DATE: 2004-06-07
PRIOR FILING DATE: 2004-06-07
PRIOR FILING DATE: 2004-06-09
NUMBER OF SEQ ID NOS: 34460
SOFTWARE: PastSEQ for Windows Version 4.0
LENGTH: 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 21;
Pred. No.
Sequence 26026, Application US/11124367A Publication No. US20060024700A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo Bapiens
US-11-124-367A-26026
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Best Local Similarity
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. RESULT 4 US-11-124-367A-26025/c

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IS-10-330-773-416/c
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LENGTH: 43103
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LENGTH: 71207
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APPLICANT: Marc Malandro.
TITLE OF INVENTION: Novel Compositions and Methods in Cancer FILE REFERENCE: 529452001300
CURRENT APPLICATION NUMBER: US/10/330,773
CURRENT PILING DATE: 2002-12-27
NUMBER OF SEQ ID NOS: 981
SOFTWARE: FatESEQ for Windows. Version 4.0
SEQ ID NO 75782
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APPLICANT: Marc Malandro
TITLE OF INVENTION: Novel Compositions and Methods in Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 610;
TITLE OF INVENILUM:
FILE REFERENCE: 108927.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT PILING DATE: 2001-08-08
PRIOR PELICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FASTESQ for WINGOWS VERSION 4.0
SEQ ID NO 546671
LENGTH: 610
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Publication No. US20060040262A1
GENERAL INFORMATION:
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; OTHER INFORMATION: n = A,T,C or G
US-10-330-773-772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
US-09-925-065A-546671
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Best Local Similarity
Matches 21; Conserv
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Score 21; DB 7; Length 390183;
Pred. No. 0.89;
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Sequence 416, Application US/10330773
Publication No. US20060040262A1
GENERAL INFORMATION:
APPLICANT: David W. Morris
APPLICANT: David W. Morris
APPLICANT: David W. Morris
APPLICANT: David W. Morris
APPLICANT: Marc Malandro
TITLE CF INVENTION: Novel Compositions and Methods in Cancer FILE REFERENCE: 529452001300
CURRENT FILING DATE: 2002-12-27
NUMBER OF SEQ ID NOS: 981
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: CARGILL, Michele et al.
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRU
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FASTSEQ for Windows Version 4.0
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NUMBER OF SEQ ID NOS: 981
SOFTWARE: PattSEQ for Windows Version 4.0
SEQ ID NO 937
LENGTH: 390183
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Publication No. US20050272054A1
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// OTHER INFORMATION: n = A,T,C or G
US-10-330-773-937
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Best Local Similarity 100.
Matches 21; Conservative
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Matches 20, Conservative
                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                       FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(39018:
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CREANISM: Homo sapiens
US-10-995-561-13346
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785 TCCTCTCCCTCTCCTCC 804
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                                                                                             RESULT 13
US-10-330-773-395/c
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i Sequence 24, Application US/10933025

j Publication No. US20050265987A1

i GENERAL INFORMATION.

APPLICANT: ROSEN, STEVEN

APPLICANT: TOMITA, MEGUMI

I TITLE OF INVENTION: Lheroef

FILE REFERENCE: UCAL-230CON

CURRENT APPLICATION UNMBER: US/10/933,025

CURRENT FILING DATE: 2004-09-01

PRIOR APPLICATION NUMBER: 10/025,966

PRIOR APPLICATION NUMBER: 60/256,77

PRIOR APPLICATION NUMBER: 60/256,77

PRIOR APPLICATION NUMBER: 60/256,77

PRIOR FILING DATE: 2000-12-27

PRIOR FILING DATE: 2000-12-27

PRIOR FILING DATE: 2001-09-02

NUMBER OF SEQ ID NOS: 26

NUMBER OF SEQ ID NOS: 26

SOFTWARE: FASTSEQ for Windows Version 4.0
               Indels
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Pred. No. 2.8; Mismatches
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                                                 785 TCCTCTCCCTCTCCTCTCC 804
Best Local Similarity 100.0%; P
Matches 20; Conservative 0;
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; ORGANISM: Mus musculus
US-10-933-025-24
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                                                                                                                                    RESULT 11
US-11-124-367A-5048/c
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LENGTH: 171936
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LENGTH: 100000
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Sequence 1382480, Application US/10310914A
Sequence 1382480, Application US/10310914A
PUDICACION NO. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06097.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SEQ TWARE: PatentIn version 3.3
SEQ ID NO 1382480
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Sequence 395, Application US/10330773
; Publication No. US2006004026241
; GENERAL INFORMATION:
   APPLICANT: David W. Morrie
; APPLICANT: Marc Malandro
   TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REPRENCE: 5.2945200130 US/10/330,773
; CURRENT APPLICATION UNBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SEQ ID NO 395
; LENGTH:::194186
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100.0%; Pred. No. ...
0; Mismatches
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Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
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NAME/KEY: misc_feature
LOCATION: (1)...(194186)
COTHER INFORMATION: n = A,T,C or G
US-10-330-773-395
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100.0%; Fre
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Best Local Similarity 100.
Matches 20; Conservative
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US-10-310-914A-1382480/c
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Matches 19; Conserv
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US-10-310-914A-1382480
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; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIÁTED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17794
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-17794

Query, Match
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Search completed: March 5, 2006, 11:44:32 Job time : 511 secs

169 CCTCTCCCTCTCCCTCTCC 187

69 8.4 560 2 BE644379 BE644379 946060P06 68 8.3 595 9 CC033608 CC033608 3591 64 67 8.1 294 5 BU093711 BU097711 3524 1 45 67 8.1 606 1 AN499193 AN499193 660043P05 67 8.1 612 5 BO485004 CC065564 BU097711 3524 1 9 67 8.1 612 5 BO485004 CC065564 BUPPO72TD 65 7.9 968 9 BZ817311 BUGCL66TD 65 7.9 968 9 BZ817318 BZ81730 BUGCL66TD 64 7.8 520 5 BO52852 BO52854 3524 1 3 64 7.8 530 5 BO528654 BO52852 3524 1 3 64 7.8 530 5 BO528654 BO52852 3524 1 3 64 7.8 531 AN499212 BO52852 3524 1 3 64 7.8 534 5 BO528654 BO57758 3524 1 3 64 7.8 574 5 BO528654 BO57768 3524 1 3 65 7.7 635 10 CG119014 BU099103 3524 1 3 65 7.7 640 1 AN499212 CC067360 BU099103 3524 1 3 65 7.7 640 1 AN499212 BU099103 AURIEN FUDBPF47B 65 7.7 641 AN499212 BU099103 AURIEN FUDBPF47B 65 7.7 641 AN499218 AN499918 GC0041G02 65 7.7 641 AN499218 AN499918 GC0041G02 65 7.7 641 AN499218 AN49918 BU099109 3524 1 3 65 7.7 640 AN499218 AN49918 BU099109 3524 1 3 65 7.7 640 AN499218 AN49918 BU099109 3524 1 3 65 7.7 640 AN499218 AN49918 BU099109 AURICATED	ALIGNMENTS	SEULT 1  COUILI45  COULLI45  COULLIAG  COULLIA
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GenCore version 5.1.7  Copyright (c) 1993 - 2006 Biocceleration Ltd.  OM nucleic - nucleic search, using sw model  Run on: March 5, 2006, 11:20:48; Search time 4129 Seconds (without alignments) 9325.689 Million cell updates/sec Title: US-10-660-208-90 Perfect score: 823 Sequence: 1 ctgcacggtactccaagtatcgatccatctccagcgcag 823 Scoring tracter of Capop 60.0, Gapext 60.0 Searched: 41078325 seqs, 23393541228 residues  Copyright (c) 1993 - 2006 Total number of hits satisfying chosen parameters: 82156650	seq length: 0 seq length: 2000000000 saing: Listing first 45 summaria	Database : EST:

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OCRAES4TV ZM 0.7_1.5 KB Zea mays genomic clone ZKWBMa0349111, genomic survey sequence.
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                                                                                                                                 152 AGCTAAGACACTGTGTCTTCGTCAAGATACATGTCTTGAGATTTTTTACATTCACCCCCC 211
                                                                                                                                                                        74 AGCTAAGACACTGTGTGTCTTCGTCAAGATACATGTCTTGAGATTTTTTACATTCACCCCC 133
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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resmick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 ACCACCCCTCGTTTATACTATATATACACAGACGCACGATACCCATATCGTGGTGCTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92 CAATCAGAACATTCAATAAATTAAAGTGACCAATCAGATAGTCTCCTGTCCCGAATATAG
                                                                             14 CAATCAGAACATTCAATAAATTAAAGTGACCAATCAGATAGTCTCCTGTCCCGAATATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:4577"
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/note="voctor: pBCSK-; Site_1: HinclI; 0.7-1.5 kb
methylation filtered genomic DNA library"
                                                                                                                                                                                                                  212 TAGACACACTCTAAGACACAACTTAAGACACCCATTGTACATGCCCTAA 260
                                                                                                                                                                                                                                       9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
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15.2%; Score 125; DB 9; I
Best Local Similarity 100.0%; Pred. No. 1.2e-57;
Matches 125; Conservative 0; Mismatches 0;
100.0%; Pred. No. 3.5e-82; ive 0; Mismatches 0;
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/strain="B73"
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1. .964
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Class: methylation filtered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2002)
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                             CC331498.1 GJ:30800669
  Best Local Similarity 100.0
Matches 169; Conservative
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CC331498
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 815)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, F., Ma, J. and
                                                              470
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                                                                                                                                                                                                                                                              360 ACTICGAGGICAGCALIGIACITITIGITAACGICICGATAAATIGITGACTIAAAATAG 419
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/note="Vector: pCR4_TOPO; Site_1: EcoRI; 0.6-1.0 kb high
CoT selected genomic DNA library"
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      CAGAAGTATTGTGGCTGCATATTGCTGAAATTATAGCGAGGGCCCAAGGCCCATCACTTC
                                                                                                                                                                                                                          531 ACTICGAGGICAGCATIGIACITITGITAACGICTCGATAAATTIGITCACTTAAAATAG
                                                                411 TAAGCAAACAAGCGAACATTGCTTAGCTACAACCAATTTGCTGGGCTTCCATGGGCATCG
                                                                                                                                             471 CAGAAGTATTGTGGCTGCATATTGCTGAAATTATAGCGAGGGCCCAAGGCCCATCACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       600 ACAGCCGAGCGATCTCCTCTCCCTCTCCCGATCCATTCTCCAGCGCAG 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   771 ACAGCCGAGCGATCTCCTCTCCCTCTCCCGATCCATTCTCCAGCGCAG 823
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Fax: 301-838-0208
Email: whitelaw@tigr.org
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/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
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Class: sheared ends.
Location/Qualifiers
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Other GSSs: PUHJY12TB
Contact: Cathy Whitelaw
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CC409846.1 GI:30889936
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CG130321 882 bp DNA linear GSS 21-AUG-2003 PUXDM45TD ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa0794H17,
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta, Liliopaida; Poales, Poaceae, PACCAD
Glade, Panicoideae, Andropogoneae, Zea.

1 (bases 1 to 882)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
                                                                                                                                   1. .894

/organism="zea mays"

/ml_type="genomic DNA"

/strain="873"

/db_xref="taxon:4577"

/clone="xeeta"vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high

CoT selected genomic DNA library"
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COT selected genomic DNA library"
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Tel: 301-838-5843
Fax: 301-838-0208
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                                                                                                                                                                                                                                                                                                                                                                                   Query Match 12.5%; Score 103; DB 9; I
Best Local Similarity 100.0%; Pred. No. 2.2e-45;
Matches 103; Conservative 0; Mismatches 0;
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/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
    Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.
Location/Qualifiers
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Seq primer: TF
Class: sheared ends.
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Other GSSs: PUKDM45TB
Contact: Cathy Whitelaw
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GAMBK41TV ZM 0.7 1.5 KB Zea mays genomic clone ZMMBMa0384G09, genomic survey sequence.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 894)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Besnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
                                                                                                                                                                                               Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoldeae, Andropogoneae, Zea.
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methylation filtered genomic DNA library"
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Unpublished (2003)
Contect: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
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Tel: 301-838-5843
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/strain="873"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'organism="Zea mays"
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Class: methylation filtered
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                                                                                                     CC331420.1 GI:30800591
GSS.
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CC356660.1 GI:30826060
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Zea mays
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Tel: 301-838-5843
Fax: 301-838-0208
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ZMMBF0140018r ZMMBF Zea mays genomic clone ZMMBF0140018 3', genomic
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144 GANTATAGAGCTAAGACACTGTGTCTTCGTCAAGATACATGTCTTGAGATTTTTTACATT 203
               Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.
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/clone="xxwhbra0794H17"
/clone="tb="zM_0.6_1.0 KB"
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COT selected genomic DNA library"
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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
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                                                                                638 CACCCCCTAGACACACTCTAAGACACACATTAAGACACCCA 679
                                                               204 CACCCCCTAGACACACTCTAAGACACAACTTAAGACACCCA
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Best Local Similarity 100.0%; Pred. No. 7.9e-45;
Matches 102; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
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Fax: 301-838-0208
Email: whitelaw@tigr.org
Seg primer: TR
Class: sheared ends.
Location/Qualifiers
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Unpublished (2003)
Other GSSs: PUKDM45TD
Contact: Cathy Whitelaw
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CZ362236/c
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CC007924 . 324 bp DNA linear GSS 31-MAR-2003
PUEBI48TD ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa197H23,
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Trachcophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea. 1 (bases i to 893) Bharti, A.K., Nelson, A.B., Young, S., Keizer, G., Zohovetz, V., Puka, G. and Messing, J.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoldeae; Andropogoneae; Zea.
1 (bases 1 to 324)
Mhitclaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
                                                                                                                                                                                                                                   Unpublished (2005)
Contact: Bharti,A.K.
Dr.Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
                                                                                                                                                                      Construction, Sequencing and Characterization of a Fosmid Library of the B73 Maize Genome
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/clone=zRMBF0140018"
/lab host="EP1100-T1"
/clone llb="ZMMBF"
/note="Vector: pEp1F0S-5; Site_1: Eco721"
                                                                                                                                                                                                                                                                                                                                                                       190 Frelinghuysen Road, Piscataway, NJ 08854, USA Tel: 732 445 3801
Fax: 732 445 5735
Bmail: bharti@waksman.rutgers.edu
Seq primer: SP6
Class: fosmid ends.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 11.8%; Score 97; DB 10; L
1 Similarity 100.0%; Pred. No. 4.8e-42;
97; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Zea mays"
/mol type="genomic DNA"
/cultivar="B73"
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Class: sheared ends.
Location/Qualifiers
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Unpublished (2003)
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/organism="Zea maye"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/cultivar="OH43"
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                                                                                              nays cDNA, mRNA sequence.
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Spermatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
1 (bases 1 to 737)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Frager, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Zea mays"
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/strain="B73"
/db_xref="taxon:4577"
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COT selected genomic DNA library"
           89
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                                                                                                                                                       Query Match 10.3%; Score 85; DB 9; Length 324; Best Local Similarity 100.0%; Pred. No. 2.3e-35; Matches 85; Conservative 0; Mismatches 0; Indels
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organism="Zea mays"
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Location/Qualifiers
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Unpublished (2003)
Contact: Cathy Whitelaw
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Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
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CC409551.1 GI:30889641
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Matches 83; Conserv
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BES10330 563 bp mRNA linear EST 07-AUG-2000 946052B01.x1 946 - tassel primordium prepared by Schmidt lab Zea
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                                                                                                                                                                                                                                                                             Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae, PACCAD clade; Panicoldeae, Andropogoneae, Zea. [ (bases 1 to 563)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'tissue type="tassels"
'dev_stage="just after the transition from·vegetative to
inflorescence development"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone_lib="946 - tassel primordium prepared by Schmidt
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Fax: 650 725 8221
Email: walbotestanford.edu
Plate: 946052 row: B column: 01.
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9.7%; Score 80; DB 2; Lv
Best Local Similarity 100.0%; Pred. No. 1.4e-32;
Matches 80; Conservative 0; Mismatches 0;
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GSS 18-JUN-2003
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                                                                                                                                                                              Eukaryota, Viridiplantae, Stréptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 902)
Whitelaw C.A., Quackenbush, J., Van Aken, S., Utterback, T., '
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., '
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
Contact: Cathy Whitelaw
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               /clone_lib="ZMMBLa"
/note="Vector: pAGIBAC1; Site_1: Sal1; Site_2: Sal1"
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                                                                                Query Match
Best Local Similarity 100.0%; Pred. No. 5.2e-32;
Matches 79; Conservative 0; Mismatches 0; Indels
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Pax: 301-838-0208
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/lab_host="DH10B Tl phage resistant"
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1. .902
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Class: methylation filtered.
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                                                                                                                                                                                                                                                      465 TCACCCCCTAGACACACT 483
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                                                                                                                                                                                                                                                                                                                                                                                                 genomic survey sequence.
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Zea mays
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CC334197/c
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Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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ZMMBL sequences
L Unpublished (2004)
Contact: Red (2004)
Contact: Red (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: rwing@genome.arizona.edu
Plate: 0009 row: E column: 11
Class: BAC ends.
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Wing,R., Luo,M., Soderlund,C. and Haller,K.
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/clone="ZMMBLa0007D24"
/tissue_type="immature ears"
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/mol_type="genomic DNA"
/cultivar="B73"
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/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
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Plate: 0007 row: D column: 24
Class: BAC ends.
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/clone="ZMMBLa0009E11"
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Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
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Matches 79; Conservative
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
Other GSSs: OGUBN60TH
Contact: Cathy Whitelaw
OGUBN60TV ZM_0.7_1.5_KB Zea mays genomic clone ZMVBMa0401J24, genomic survey sequence.
CC607552
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/note="Vector: pBCSk-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
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Class: methylation filtered.
Location/Qualifiers
1. 902
/ organism="Zea mays"
/mol type="genomic DNA"
/strāin="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone="ZMMBMa0401J24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: whitelaw@tigr.org
                                                                   CC607552.1 GI:31968973
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203 TCACCCCCTAGACACACT 221 563 TCACCCCCTAGACACACT 581 ð

503 GGAATATAGAGCTAAGACACTGTGTCTTCGTCAAGATACATGTCTTGAGATTTTTTACAT 562

143 CGAATATAGAGCTAAGACACTGTGTCTTCGTCAAGATACATGTCTTGAGATTTTTTACAT 202

0; Gaps

Search completed: March 5, 2006, 14:56:37 Job time : 4131 secs

Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence

Sequence Sequence Sequence

Sequence Sequence Sequence Sequence Sequence

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APPLICANT: Schnable, Patrick S.
APPLICANT: Robertson, Donald S.
APPLICANT: Hansen, Joel D.
APPLICANT: Nikolau, Basll J.
APPLICANT: Xu, Xiaojie
APPLICANT: Xu, Xiaojie
TITLE OF INVENTION: ISOLATION AND USE OF CUTICULAR LIPID
TITLE OF INVENTION: GENES
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Marrier
STREET: Two Prudenti
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COMPUTE: IBM PC Compatible
SPERATING SYSTEM: PC-DGS/MS-DOS
SPETWARE: PATENTINE Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/581,148C
FILING DATE: 29-DEC-1995
CLASSIPICATION NUMBER: 35243
REFERMENT APPLICATION NUMBER: 35243
REFERMENCE DOCKET NUMBER: 71380
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEPHONE: (312) 616-5700
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
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COUNTRY: US
ZIP: 60601-6780
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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LYPE: nucleic acid
TYPE: nucleic acid
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334
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33769
34414
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INDIVIDUAL ISOLATE:
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March 5, 2006, 08:22:14; Search time 878 Seconds
   (without alignments)
1666.211 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 53357, 1
Sequence 15354, 1
Sequence 13139, 1
Sequence 13025, 1
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           GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cgn2_6/ptodata/1/ina/1_COMB.seq:*
/cgn2_6/ptodata/1/ina/5_COMB.seq:*
/cgn2_6/ptodata/1/ina/6_COMB.seq:*
/cgn2_6/ptodata/1/ina/H_COMB.seq:*
/cgn2_6/ptodata/1/ina/H_COMB.seq:*
/cgn2_6/ptodata/1/ina/H_COMB.seq:*
/cgn2_6/ptodata/1/ina/PP_COMB.seq:*
/cgn2_6/ptodata/1/ina/PP_COMB.seq:*
/cgn2_6/ptodata/1/ina/PP_COMB.seq:*
/cgn2_6/ptodata/1/ina/PP_COMB.seq:*
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                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                   1303057 segs, 888780828 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                           OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Issued Patents NA:
                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                       US-10-660-208-90
823.
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Match Length DB
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102053
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                                                                                                             Run on:
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No.
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Gaps
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3.9%; Score 32; DB 3; Length 6550;
Best Local Similarity 100.0%; Pred. No. 5.9e-07;
Matches 32; Conservative 0; Mismatches 0; Indels
                                                                                                              join(4201..4425, 5059..5250, 5383..5547, 5649
..6068)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/643,971
                                                                                                                                                                                                                                                                                       1415 rcraaaacarcrecrraccararrcarrera 1446
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OTHER INFORMATION: /product= "Peroxidage"
                                                                                                                                                                                                                                                      59 TCTAAAACATGTGTCTTACCATATTCATTGTA 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: DowElanco Patent Department STREET: 9330 Zionsville Road CITY: Indianapolis
                                                                                                                                                                                                                                                                                                                                            US-09-643-971-1

Sequence 1, Application US/09643971

Patent No. 6699984

GENERAL INFORMATION:

APPLICANT: Affiley, Michael

APPLICANT: Armstrong, Katherine
                                                                                                                                                                                                                                                                                                                                                                                                                             Ainley, Michael
Armstrong, Katherine
Belmar, Scott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Stuart, Donald R
TELECOMUNICATION INFORMATION:
TELEPHONE: 317 337 4816
TELEPAK: 317 337 4817
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hopkins, Nicole
Menke, Michael A.
Pareddy, Dayakar
Petolino, Joseph F
Smith, Kelley
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4426..5058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: exon
FOCATION: 4201..4425
                5549..5649
                                                                  5650..6065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: doubl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
LOCATION:
FEATURE:
                                              | NAME/KEY:
| FLOCATION:
| FEATURE:
| NAME/KEY:
| LOCATION:
| LOCATION:
| UCS-109-097-319A-1
NAME/KEY:
LOCATION:
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Woosley, Aaron
TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                              Length 6343;
                                                                   0; Indels
                                                                                                                       3715 CATTCAATAAATTAAAGTGACCAATCAGATAGTCTC 3750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 46268

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,319A
                                                                                                    101 CATTCAATAAATTAAAGTGACCAATCAGATAGTCTC 136
                                 Query Match
4.4%; Score 36; DB 3; Lt
Best Local Similarity 100.0%; Pred. No. 3.9e-09;
Matches 36; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 4201..4425
OTHER INFORMATION: /product= "Peroxidase'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: DowElanco Patent Department 9330 Zionsville Road
                                                                                                                                                                                                                    Sequence 1, Application US/09097319A Patent No. 6384207
                                                                                                                                                                                                                                                                          Ainley, Michael
Armstrong, Katherine
Belmar, Scott
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Hopkins, Nicole
Menke, Michael A.
Pareddy, Dayakar
Petolino, Joseph F.
Smith, Kelley
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ATTORNEY/AGENT INFORMATION:
NAME: Stuart, Donald R
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317 337 4847
TELEFAX: 317 337 4847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 6550 base pairs
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4426..5058
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.5059.,5250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5251..5382
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5383..5548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Indiana
COUNTRY: USA
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LOCATION:
FEATURE:
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LOCATION:
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LOCATION:
FEATURE:
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LOCATION:
FEATURE:
   US-08-581-148C-30
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APPLICANT:
APPLICANT:
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Sequence 16, Application US/09097319A Patent No. 6384207 GENERAL INFORMATION:
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TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 317 337 4847
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 TCTAAAACATGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 9330 Zionsvi
CITY: Indianapolis
STATE: Indiana
COUNTRY: USA
 ; MOLECULE TYPE: DNA US-09-097-319A-15
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Matches 32; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
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US-09-097-319A-16
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US-09-643-971-15
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VENTION: Regulatory Sequences for Transgenic Plants
                                                                                                                                                                                                                                                                                                                                               Ouery Match 3.9%; Score 32; DB 3; Length 6550; Best Local Similarity 100.0%; Pred. No. 5.9e-07; Matches 32; Conservative 0; Mismatches 0; Indels
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..6068)
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,319A
                                                                                                                                                                                                                                                                                                                                                                                                                       59 TCTAAAACATGTGTCTTACCATATTCATTGTA 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pplication US/09097319A
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Armstrong, Katherine
Belmar, Scott
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ATTORNEY/AGENT INFORMATION:
NAME: Stuart, Donald R
TELECOMUNICATION INFORMATION:
TELEPHONE: 317 337 4816
TELEPAX: 317 337 4847.
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   exon
5059..5250
                                                                  5251..5382
                                                                                                                     5383..5548
                                                                                                                                                                       5549..5649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
                                                                                                                                                                                                                             5650..6065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 46268
COMPUTER READABLE FORM:
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                                                    intron
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                                                                                                                                                                                                                                                          ) NAME/KEY:
; LOCATION:
; LOCATION:
US-09-643-971-1
NAME/KEY:
LOCATION:
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LOCATION:
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LOCATION:
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TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
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Score 32; DB 3; Length 9299;
Pred. No. 5.9e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 9299;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/643,971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 32; DB 3; I
Pred. No. 5.9e-07;
                                                                                                                                    1462 rcraaacarcrerrraccararrcarrera 1493
Query Match 3.9%; Score 32; DB Best Local Similarity 100.0%; Pred. No. 5.9 Matches 32; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DowElanco Patent Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                            Sequence 15, Application US/09643971 Patent No. 6699984
                                                                                                                                                                                                                                                                                                              Ainley, Michael
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Stuart, Donald R
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317 337 4816
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US-09-950-933A-8
US-09-950-933A-8
Sequence 8, Application US/09950933A
Sequence 8, Application US/09950933A
GENERAL INFORMATION:
APPLICANT: Simmons, Carl R.
APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: Autimicrobial Peptides and Methods of TITLE OF INVENTION: Antimicrobial Peptides and Methods of TITLE OF INVENTION: US-09-09-13
CURRENT FILING DATE: 2001-09-11
PRIOR PILING DATE: 2000-09-13
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: NA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 9408;
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                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
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Pred. No. 5.9e-07;
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Pred. No. 7e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1468 TCTAAAACATGTGTCTTACCATATTCATTGTA 1499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 3.9%; Score 32; DB Best Local Similarity 100.0%; Pred. No. 5.9 Matches 32; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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Patent No. 6812339
GENERAL INFORMATION:
                                                                                                                                                                                                                                      NAME: Stuart, Donald R
FELECOMMUNICATION INFORMATION:
TELEPHONE: 317 337 4816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.6%;
                                                                                                                                                                                                CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Stuart, Donald R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                     TELEFAX: 317 337 4847 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS LENGTH: 9408 base pai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: CDS
; LOCATION: (119)...(403)
US-09-950-933A-8
                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: doub
TOPOLOGY: circular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Zea mays
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    COUNTRY:
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                                                                                                                        TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants NUMBER OF SEQUENCES: 59 CORRESPONDENCE ADDRESS: DOWELAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Woosley, Aaron
WTMTION: Regulatory Sequences for Transgenic Plants
SOURNDES: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 9408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,319A FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 3.9%; Score 32; DB 3; Le
Best Local Similarity 100.0%; Pred. No. 5.9e-07;
Matches 32; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                             E: DowElanco Patent Department 9330 Zionsville Road
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Patent No. 6699984
GENERAL INFORMATION:
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Armstrong, Katherine
Belmar, Scott
Ainley, Michael
Armstrong, Katherine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Stuart, Donald R
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317 337 4816
TELEFAX: 317 337 4847
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 9408 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9330 Zionsville Road
                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible
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Smith, Kelley
                                                               Folkerts, Otto
Hopkins, Nicole
Menke, Michael A.
Pareddy, Dayakar
Petclino, Joseph F
Smith, Kelley
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lopkins, Nicole
                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: doubl
                                                                                                                                                                                                                                                                                                       CITY: Indianapolis
STATE: Indiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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APPLICANT: Woosley
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                   46268
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
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Best Local Similarity 100.
Matches 21; Conservative
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Best Local Similarity 100.
Matches 21; Conservative
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US-09-949-016-53357
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US-09-949-016-15354
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Facent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: 00/24-14

FRIOR APPLICATION NUMBER: 60/24,755

FRIOR PELING DATE: 2000-10-20

FRIOR PELING DATE: 2000-10-03

FRIOR PELING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FEASTSEQ for Windows Version 4.0

SEQ ID NO 17302
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILLE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR PPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12542
LENGTH: 173787
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Best Local Similarity 100.
Matches 22; Conservative
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Best Local Similarity 100.
Matches 22; Conservative
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US-09-949-016-12542
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WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS
TITLE OP INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REPERENCE: CL001307
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
PRIOR PILING DATE: 2000-09-08
PRIOR PLING DATE: 2000-09-08
SOFTWARE: PastSEQ for Windows Version 4.0
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN G.
FILLE OF INVENTION: WITH HUMAN DISEASE, MET
FILLE OF INVENTION: WITH HUMAN DISEASE, MET
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR PELICATION NUMBER: 60/231,758
PRIOR PELICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
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SOFTWARE PSSTSEQ for Windows Version 4.0
SEQ ID NO 15354
LENGTH: 37385
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Pred. No.
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CURRENT FILING DATE: 2000-04-14
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Patent No. 6812339
GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NOS: 207012
SEQ ID NOS: 207012
SEQ ID NOS: 207012
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US-09-949-016-15824, Application US/09949016
Sequence 15824, Application US/09949016
Sequence 15824, Application US/09949016
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERBRUGE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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2.6%; Score 21; DB 3; Length 102053;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 21; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                   Length 95648;
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2.6%; Score 21; DB 3;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 21; Conservative 0; Mismatches
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13139
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US-09-949-016-13025/c
Sequence 13025, Application US/09949016
; Patent No. 6812339
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PRIOR APPLICATION NUMBER: 60/241,755
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| LOCATION: (1)...(102053)
| OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13025
                                                                                                                                                                                                                                                               | NAME/KEY: misc_feature
| LOCATION: (1)...(95648)
| OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13139
                                                                                                                                                                                TYPE: DNA
ORGANISM: Human
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ORGANISM: Human
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Aal37816 Corn KCP-
Adx53136 Plant ful
Aas96543 Primer #6
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                                                                   OM nucleic - nucleic search, using sw model
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ADX53136
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ADX49209
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ADX60974
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ADX48086
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## ALIGNMENTS

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Corn, male reproductive tissue, plant regulatory sequence, Zea mays, promoter, transcription regulation, operably linked gene, monocot, dicot, wheat anther, plant fertility; insect tolerance, pathogen tolerance, herbicide tolerance, ds.
                                                                                                                                                                                                                                                                                                                                                               Novel promoters isolated from corn for controlling gene expression in male reproductive tissues, such as anthers, tassels, and to regulate transcription of target genes including genes for insect or pathogen tolerance.
                                                                                                                                                                                                                                                                                                                        Masucci JD,
                                                                                                                                                                                                                                                                                                                      Conner TW, Dubois P, Malven M,
                                                                                                                                                                                                                                                                                               (MONS ) MONSANTO TECHNOLOGY LLC
                      AAS96569 standard; DNA; 823 BP.
                                                                                                                                                                                                                                                                    01-MAY-2000; 2000US-0201255P.
                                                                                                                                                                                                                                                 30-APR-2001; 2001WO-US013739.
                                                                                           Corn promoter sequence #12.
                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                              WPI; 2002-055481/07.
                                                                                                                                                                                                  WO200183790-A2.
                                                                    26-FEB-2002
                                                                                                                                                                                                                          08-NOV-2001:
                                             AAS96569;
                                                                                                                                                                             Zea mays.
           AAS96569
RESULT
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The present invention relates to the isolation of plant regulatory sequences from the male reproductive tissues of corn (Zea mays). The promoter sequences, fragments, regions or cis elements of the sequences, are capable of regulating transcription of an operably linked DNA

Claim 1, Page 113-114; 121pp; English.

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sequence. The promoter sequences confer enhanced expression of operably linked genes in monocot or dicot male reproductive tissues, such as anthers, especially wheat anthers and is useful for regulating transcription of a DNA sequence, by operably linking the DNA sequence the promoter. The promoter sequences are useful in plants to regulate transcription of target genes including genes for control of fertility, insect or pathogen tolerance and herbicide tolerance. They are also useful as probes or primers in nucleic acid hybridisation experiments. The promoter sequences can be used in hybridisation assays of other plant tissues to identify closely related or homologous genes and associated regulatory sequences. AAS96558-AAS96577 represent the corn promoter
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Local Similarity 100.0%; Pred. No. 0;
168 823; Conservative 0; Mismatches
                                                                                                                                                 regulatory sequences. AAS96558-AAS9
sequences of the present invention
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The present invention relates to the isolation of plant regulatory sequences from the male reproductive tissues of corn (Zea mays). The promoter sequences, regions or cis elements of the sequences, are capable of regulating transcription of an operably linked DNA sequence. The promoter sequences confer enhanced expression of operably linked DNA sequence. The promoter sequence, by operably linking the DNA sequence and is useful for regulating the DNA sequence. The promoter sequences are useful in plants to regulate transcription of a DNA sequence, by operably linking the DNA sequence to the promoter. The promoter sequences are useful in plants to regulate transcription of target genes including genes for control of fertility, insect or pathogen tolerance and herbicide tolerance. They are also useful as probes or primers in nucleic acid hybridisation assays of other plant the promoter sequences can be used in hybridisation assays of other plant tissues to identify closely related or homologous genes and associated transcription sequences.
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                                                                                                                                                                                                                    Corn; male reproductive tissue; plant regulatory sequence; Zea mays; promoter; transcription regulation; operably linked gene; monocot; dicot; wheat anther; plant fertility; insect tolerance; pathogen tolerance; herbicide tolerance; ds.
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                                                                                       standard; DNA; 1587
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
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01-APR-1999;
06-APR-1999;
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19-APR-1999;
21-APR-1999;
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99US-0161404P.
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99US-0161406P.
99US - 0145919P.
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04-AUG-1999;
04-AUG-1999;
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17-AUG-19
18-AUG-19
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New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for improving yield.
                                                                                                                                                    749 GIGGIGCIAGAAGCAACIGAAAACAGCCGAGCGAICICCTCCCTCTCCCTCTCCCGAIC 808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention describes a recombinant DNA construct comprising a polymucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polymucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                     plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; och tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; yalatcomanan production; pathway; disease resistance; yield; plant growth; plant development; seed oil; protein yield; protein yield;
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                                                                                                    Length 769
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                                                                                                                                                                                                                                                                                                                                                                                 Plant full length insert polynucleotide segid 23949.
                                                                                                   9.0%; Score 74; DB 3; L. 100.0%; Pred. No. 2.4e-28; ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                           )209/c
ADX49209 standard; cDNA; 485 BP.
99US-0161359P.
99US-0161360P.
99US-0161361P.
99US-0161920P.
99US-0161993P.
99US-0161993P.
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                                                                                                Query Match
Best Local Similarity 100. Marches 74; Conservative
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ZHOU Y.
KOVALIC D K.
SCREEN S E.
TABASKA J E.
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26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
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(ZHOU/)
(KOVA/)
(SCRE/)
(TABA/)
(CAOY/)
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                       improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, lighin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert polynucleotide that can be used in the recombinant DNA construct of the
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            plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme
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Pred. No.
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05-NOV-2001; 2001US-00985678.
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Best Local Similarity 100.
Matches 63; Conservative
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                                                                                                                                                                                                                       nvention
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(ZHOU/)
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ADX33652
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                                                                                          The invention describes a recombinant DNA construct comprising a polymucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from 1900 yearent office at ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polymucleotide of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, lighin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of
                                                                                                                                                                                                                                                                                                                                photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert polymucleotide that can be used in the recombinant DNA construct of the
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pests, for conferring increased resistance to plant disease, or for improving yield.
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100.0%; Pred. No. 5.7e-22;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 821 BP; 187 A; 227 C; 214 G; 193 T; 0 U; 0 Other;
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                                                       Claim 1; SEQ ID NO 16472; 15pp; English
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05-NOV-2001; 2001US-00985678.
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Best Local Similarity 100.1
Matches 62; Conservative
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SCREEN S E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ZHOU/)
(KOVA/)
(SCRE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
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The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at trp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant colerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, increased resistance to plant disease, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one careas condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert property of the content. This sequence represents a plant full length insert of the
                                                                                                                                                                        New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens pests, for conferring increased resistance to plant disease, or for improving yield.
                                                                         Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 791 BP; 181 A; 215 C; 215 G; 180 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 12914; 15pp; English.
(TABA/) TABASKA J E.
(CAOY/) CAO Y.
                                                                                                                          WPI; 2004-180133/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention
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0; Сарв Query Match
7.2%; Score 59; DB 13; Length 791;
Best Local Similarity 100.0%; Pred. No. 2.2e-20;
Matches 59; Conservative 0; Mismatches 0; Indels

765 CIGAAAACAGCCGAGCGAICTCCTCTCCCTCTCCCGAICCAITCTCCAGCGCAG 823 CTGAAAACAGCCGAGCGATCTCCTCTCCCTCTCCCTCCCGATCATTCTCCAGCGCAG 59 ò 유

ADX30071 standard; cDNA; 795 BP 21-APR-2005 (first entry) ADX30071; 

Plant full length insert polynucleotide seqid 12891.

plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; pest tolerance; all cycle pathway; disease resistance; yield; plant growth; plant development; seed oil; protein yield; protein content; gene; ss.

Unidentified

US2004034888-A1

19-FEB-2004

28-APR-2003; 2003US-00425114

06-MAY-1999; 99US-00304517, 05-NOV-2001; 2001US-00985678.

Ω TABASKA J KOVALIC D SCREEN S LIU J. ZHOU Y. (SCRE/) (TABA/) (CAOY/) (/min KOVA/) ZHOU/ 

Cao Y; Таравка ЈЕ, Zhou Y, Kovalic DK, Screen SE, Liu J,

G K

WPI; 2004-180133/17.

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New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for improving yield.

Claim 1; SEQ ID NO 12891; 15pp; English.

The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at the sequence is uspto:gov/sequence.html?DocID:2004034888; The polynucleotide of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, hearbicides, extreme improving plant tolerance to cold, heat, drought, hearbicides, extreme improving plant tolerance to cold, heat of manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistence to plant disease, for moreasing the rate of homologous recombination in plants, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one arress condition or for modifying seed oil or pictein yield and/or content. This sequence represents a plant full length insert polynucleotide that can be used in the recombinant DNA construct of the nvention

Sequence 795 BP; 181 A; 215 C; 215 G; 184 T; 0 U; 0 Other;

0, Gape 7.2%; Score 59; DB 13; Length 79: 100.0%; Pred. No. 2.2e-20; iive 0; Mismatches 0; Indele 59; Conservative Similarity Query Match Local Matches

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Length 795;

823 59 765 CTGAAAACAGCCGAGCGATCTCCTCTCCCTCTCCCGATCCATTCTCCAGCGCAG crisialalacadecealecearcrecererecererecearcearrerecadedea ò 셤

ADX33856 standard; cDNA; 781 BP

21-APR-2005 (first entry)

Plant full length insert polynucleotide segid 16676.

plant protectant, plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array, plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle.pathway; disease resistance; yalacteranman production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield; protein yield; 

Unidentified

US2004034888-A1.

19-FEB-2004

99US-00294093. 98US-0082567P.

16-APR-1999; 21-APR-1998;

13-DEC-2001

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New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention describes a recombinant DNA construct comprising a polymucleocide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at ftp. seqdata.uspto.gov/sequence.html?DocID:2004034888. The polymucleotide of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistence to plant disease, for producing galactomannan, lightin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert polynucleotide that can be used in the recombinant DNA construct of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1, SEQ ID NO 16676; 15pp; English.
                                                       06-MAY-1999; 99US-00304517.
                    28-APR-2003; 2003US-00425114
                                                                                                                                                                                                                                                         Kovalic DK,
                                                                                                                                                        KOVALIC D K. SCREEN S E.
                                                                                                                                                                                                                                                                                                WPI; 2004-180133/17.
                                                                                                                                                                                               TABASKA J
                                                                                                                                                                                                                                                         Zhou Y,
                                                                                                                                                                                                                                                                                                                                                                                                 improving yield.
                                                                                                                                                                                                                      CAO Y.
                                                                                                                 LIUJ/)
                                                                                                                                                                                                                    (CAOY/)
                                                                                                                                                                                               (TABA/)
                                                                                                                                                                             SCRE/
                                                                                                                                                                                                                                                         Liu J,
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Tabaska JE,

Gaps ö Sequence 781 BP; 175 A; 216 C; 209 G; 181 T; 0 U; 0 Other; Indels Match 6.0%; Score 49; DB 13; L Local Similarity 100.0%; Pred. No. 4.5e-15; es 49; Conservative 0; Mismatches 0; Query Match Best Local S Matches 49 셤

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## 1 CCGAGCGATCTCCTCTCCCTCTCCCATCCATTCTCCAGCGCAG 49

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ABL76691 standard; cDNA; 307
                  14-MAY-2002
            ABL76691;
RESULT 9
   ABL76691
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(first entry)

Corn tassel-derived polynucleotide (cdps) SEQ ID NO:6065.

Corn, corn tassel-derived polynucleotide, cdps, hybrid breeding, CDPs inheritance, characteristic, growth, development; disease resistance; environmental adaptability; quality, yield; molecular marker; multigene trait; plant breeding; corn tassel; gene; ss.

Zea mays

US2001051335-A1

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polymucleotide sequence (cdps) comprising a nucleic acid sequence selected from those given in ABL70627 to ABL76813. The cdps sequences encode corn tassel-derived polympetides (CDPs). The cdps sequences can be used for determining altered gene expression, to recover regulatory elements and to follow inheritance of desirable characteristics through hybrid breeding programs. (I) are also useful in the evaluation, and alteration of desired characteristics associated with growth and development, disease resistance, environmental adaptability quality and yield, and as molecular markers for studying inheritance of a tassel-specific profile of gene transcription, a transcript image, to clone regulatory elements for use in transformation vectors, to express a polypoptide, to identify, isolate or extend identical or related corn tassel nucleic acid sequences from DNA libraries, in nucleic acid
                                                                                                                                                                                                                                                                    Novel purified corn tassel-derived polynucleotide useful for determining altered gene expression, to recover regulatory elements and to follow inheritance of desirable characteristics through hybrid breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hybridisation or amplification technologies, as query sequences to determine homology of known sequences, as probe for use in Southern Northern hybridisation, and to identify the presence of and/or to determine the degree of similarity between two (or more) nucleic aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                               present sequence describes a purified corn tassel-derived
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 307 BP; 63 A; 99 C; 81 G; 50 T; 0 U; 14 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 40; DB 6; L
Pred. No. 2.6e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 Similarity 100.0%; Pred. No. 2.6
40; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 6065; 201pp; English.
                                                                                                                                                                                            Sherman BK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.94;
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                                                                                                                                                                                            Ito LY,
                                                                                                             LALGUDIRV.
                                                                                                                                                     SHERMAN B K.
                                                                                                                                                                                                                                 VPI; 2002-163647/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                             (LALG/)
(ITOL/)
(SHER/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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ADX60974 standard, cDNA; 1326 (first entry) 21-APR-2005 ADX60974;

Plant full length insert polynucleotide seqid 31817.

plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield; 

protein content; gene; ss

Unidentified

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The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at try. seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, ignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photogonyntheals or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content this sequence represents a plant full length insert of the
                                                                                                                                                                                                                                                                                                                                                             New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protectant; plant growth regulant; gene therapy; plant;
                                                                                                                                                                                                                                                                                           Cao Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 40; DB 13; Length 1326;
Pred. No. 2.7e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1326 BP; 353 A; 297 C; 299 G; 377 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tabaska JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plant full length insert polynucleotide seqid 16647.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48 CAGTGGTCATGTCTAAAACATGTGTCTTACCATATTCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Pred. No. --
                                                                                                                                                                                                                                                                                             Screen SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 31817; 15pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADX33827 standard; cDNA; 782 BP
                                                                                    28-APR-2003; 2003US-00425114.
                                                                                                                                                                                                                                                                                             Kovalic DK,
                                                                                                                  06-MAY-1999; 99US-00304517
05-NOV-2001; 2001US-00985678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                content. This sequence repr
polynucleotide that can be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                          KOVALIC D.K.
                                                                                                                                                                                                                         SCREEN S E.
TABASKA J E.
                                                                                                                                                                                                                                                                                                                                                                                                                        improving yield.
                                                                                                                                                                                                                                                                                               zhou Y,
                US2004034888-A1
                                                                                                                                                                                      ZHOU Y
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                                                                                                                                                                                                          (KOVA/)
(SCRE/)
(TABA/)
(CAOY/)
                                                                                                                                                                         LIUJ/)
                                                                                                                                                                                                                                                                                                 Liu J,
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                                                                                                                                                                                           ZHOU/
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ADX33827
ID ADX33
XX
AC ADX33
XX
XX
DT 21-AE
XX
KW Plant
XX
KW Plant
XX
KW cold
KW extre
KW growt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polynucleotide that can be used in the recombinant DNA construct of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens pests, for conferring increased resistance to plant disease, or for improving yield.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gape
galactomannan production, lignin production, plant growth regulator, yield, plant growth, plant development, seed oil; protein yield; protein content, gene; 88.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cao Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 782 BP; 177 A; 214 C; 207 G; 184 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tabaska JE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.4%; Score 36; DB 13;
100.0%; Pred. No. 3.5e-08;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       788 ICTCCCTCTCCCTCTCCGATCCATTCTCCAGCGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TCTCCCTCTCCCTCTCCGATCCATTCTCCAGCGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Screen SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1, SEQ ID NO 16647; 15pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liu J, Zhou Y, Kovalic DK,
                                                                                                                                                                                                                  28-APR-2003; 2003US-00425114
                                                                                                                                                                                                                                                                             05-NOV-2001; 2001US-00985678
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                                                                                                                                                                                                                                                                                                                       LIU J.
ZHOU Y.
KOVALIC D K.
SCREEN S E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-180133/17.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                            TABASKA J E
                                                                                                                                     JS2004034888-A1.
                                                                                                                                                                                                                                                                                                                                                                                                          (TABA/) TABASK
(CAOY/) CAO Y.
                                                                                              Unidentified
                                                                                                                                                                                                                                                              06-MAY-1999;
                                                                                                                                                                             9-FEB-2004.
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                                                                                                                                                                                                                                                                                                                                                                     (KOVA/)
(SCRE/)
                                                                                                                                                                                                                                                                                                                         LIUJ/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADX48086/c
ID ADX4808
XX ADX480
XX DT 21-APR
XX XX
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Maize, glossy2; gl2; cuticle, cuticular lipid biosynthesis; lipid composition; lipid quantity; disease resistance, pest resistan wind resistance; frost resistance; UV resistance; transgenic plant; antisense inhibition; ds

10-OCT-2000 (first entry)

Maize glossy2 (gl2) gene.

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New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for
       recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield; protein content; gene; ss.
                                                                                                                                                                                                                                                                             Tabaska JE,
                                                                                                                                                                                                                                                                           Screen SE,
                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 22826; 15pp; English
                                                                                                                                                   28-APR-2003; 2003US-00425114.
                                                                                                                                                                                                                                                                           Kovalic DK,
                                                                                                                                                                      06-MAY-1999; 99US-00304517.
                                                                                                                                                                                                                                 SCREEN S E.
TABASKA J E.
CAO Y.
                                                                                                                                                                                                                          KOVALIC D K.
                                                                                                                                                                                                                                                                                               WPI; 2004-180133/17.
                                                                                                                                                                                                                                                                           Zhou Y,
                                                                                                                                                                                                                                                                                                                                                  improving yield.
                                                                                                            JS2004034888-A1.
                                                                                                                                                                                                   ZHOU Y.
                                                                                        Unidentified
                                                                                                                                19-FEB-2004
                                                                                                                                                                                                                                 (SCRE/)
(TABA/)
(CAOY/)
                                                                                                                                                                                                     (/min
                                                                                                                                                                                                                                                                           Liu J,
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Transforming plants such as maize and canola, for producing new plant varieties having disease and pest resistance involves introducing cuticular lipid genes into the plant genome.

Example 7; Col 115-122; 69pp; English

Hansen JD

Robertson DS,

Xu X, Xia Y,

Nikolau BJ,

Schnable PS,

WPI; 2000-349707/30.

(IOWA ) UNIV IOWA STATE RES FOUND INC.

95US-00581148.

29-DEC-1995;

JS6060644-A 09-MAY-2000

Zea mays.

24-MAR-1994;

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The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form trom the US patent office at ftp. seqdata.uspto.gov/sequence.html?DociD:2004034888. The polynucleotide of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for increased resistance to plant disease, for increasing the rate of homologous lightin or plant growth regulators, for increasing the rate of homologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    content. This sequence represents a plant full length insert polynucleotide that can be used in the recombinant DNA construct of the
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AAV63717;
                                                                   요
                                              ö
                      Length 1578;
Sequence 1578 BP; 380 A; 391 C; 429 G; 378 T; 0 U; 0 Other;
                                             Indels
                                                                    · 148 ATAGAGCTAAGACACTGTGTGTTTCGTCAAGATACAT 183
                                                                                           908 Aragagcraagacacrgrgrcrrcgrcaagaracar 873
                    4.4%; Score 36; DB 13; I 100.0%; Pred. No. 3.6e-09; tive 0; Mismatches 0;
                               Local Similarity 100.
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Query Match Best Local S Matches 36

AAA57891 standard; DNA; 6343 BP

RESULT 13 AAA57891 ID AAA XX AC AAA

g

AAA57891

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The invention relates to transforming a plant cell with either a nucleic acid encoding a plant cuticular lipid biosynthetic protein, or an acid encoding a plant cuticular lipid genese nucleic acid sequence targetted to a plant cuticular lipid gene, and then generating a plant from the plant cell. The cuticular lipid genes that may be used in the invention are given in AAA57811.

A5784 and AAA57891. The cuticle consists of a meshwork (cutin) of cross-ceterified polymerised hydroxy-fatty acids embedded in a complex mixture of nonpolar lipids (the cuticular wax). The cuticle protects and strengthens the plants, prevents evaporation of internal fluids and filters by radiation. Mutations in the cuticular lipids genes affects the quantity and composition of cuticular lipids; in maize, 17 loci (the glossy (gl) genes) have been identified as being in involved in cuticular lipid biosynthesis or control. The method is useful for introducing a lipid biosynthesis or control. The method is useful for introducing a conton, safflower, peant, palm or sunflower plant and generating a plant from the plant cell The transformed plants have improved environmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bacterial or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6343 BP; 1493 A; 1667 C; 1607 G; 1564 T; 0 U; 12 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           viral disease resistance, pest resistance, and altered lipid seeds. The present sequence represents the maize glossy2 (gl2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 6343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                resistance relating to wind, frost, UV or drought, fungal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maize per5 root preferential cationic peroxidase gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3715 CATTCAATAAATTAAAGTGACCAATCAGATAGTCTC 3750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 CATTCAATAAATTAAAGTGACCAATCAGATAGTCTC 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.4%; Score 36; DB 3; Le
100.0%; Pred. No. 3.7e-08;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAV63717 standard; DNA; 6550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-APR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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XX8XELLLLLLL

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This is the nucleotide sequence of the maize per5 root preferential cationic peroxidase gene, which encodes a 333-amino acid peroxidase cationic peroxidase conjugate the sequences a polypeptide (see AAW8783). Genomic clones comprising per5 sequences were isolated from a maize W22 genomic clones comprising per5 sequenced to per5 cDNA. Overlapping subfragments of the gene were sequenced to determine the complete 6550 by sequence of the per5 gene. Regulatory sequences derived from the per5 gene, including the promoter, introns and 3 untranslated region (3'UTR), are used in claimed recombinant gene cassettes for controlling expression of recombinant gene in selected tissue, especially the root, of transformed plants, particularly maize. The gene cassettes can be used for expression of heterologous genes such as those that confer tolerance to herbicides, insects or viruses, and genes that provide improved nutritional value or processing characteristics to the plant. Use of the per5 3'UTR sequences provides
sequence is specifically claimed in Claim 2"
                                                                                                                                                  /*tag= y
/note= "transcription termination sequence, specifically
claimed in Claim 3"
                                                           note= "this intron is specifically claimed in Claim 2" (650. .6065
                                                                                                                                                                                                                                                                                                                                                                               Menke MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated regulatory sequences for transgenic plants - which are derived from the maize root preferential cationic peroxidase protein (per5) gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6550 BP; 1844 A; 1427 C; 1346 G; 1933 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                             Folkerts O, Hopkins N, Woosley A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 6550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 32; DB 2; Len
Pred. No. 4.9e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1415 TCTAAAACAIGIGICTTACCATATTCATIGTA 1446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 TCTAAAACATGTGTCTTACCATATTCATTGTA 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.9%; Score 32; DB Best Local Similarity 100.0%; Pred. No. 4.9 Matches 32; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 84-89; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                               Belmar S,
Smith K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAV63730 standard; DNA; 9299 BP.
                                                                                                                                                                                                                                                                                                                  97US-0049752P.
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                                                                                                                                                                                                                                                                                  98WO-US011921
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/number= 4
6068. .6431
                                                    number= 3
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                                                                                                                                                                                                                                                                                                                                                                                 Armstrong K,
Petolino JF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vector plasmid PerGUS16
                                     *tag=
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P-PSDB; AAW87893.
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                                                                                                                                                                                                                                                                                  10-JUN-1998;
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                                                                                                                                                                                                                    109856921-A1
                                                                                                                                                                                                                                                                                                                                                                                 Ainley M, /
Pareddy D,
                                                                                                                                                                                                                                                     7-DEC-1998
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                       intron
                                                                                                                                   3'UTR
                                                                                        exon
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ID AAV6
XX
AC AAV6
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DT 12-3
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*tag= o
note= "this sequence is specifically claimed in Claim 2"
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//note= "this sequence is specifically claimed in Claim 2"
//stag= x
/*tag= x
          Peroxidase; per5 gene; maize; corn; transgenic plant; promoter; root; ds
                                                                                                                                                                                    . 4148
tag= b
note= "this region is specifically claimed in Claim 1"
                                                                                                                                                                                                                                                                                                                                                                                    187. .4215
trag= i
note= "this region is specifically claimed in Claim 1"
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                                                                                                       *tag= a
note= "this region is specifically claimed in Claim 1"
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note= "this region is specifically claimed in Claim 1"
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187. .4148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tag= g
note= "this region is specifically claimed in Claim 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note = "this region is specifically claimed in Claim 1"
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number=11
note= *this intron is specifically claimed in Claim
059. .5250
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number= 2
note= "this intron is specifically claimed in Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   roduct= "peroxidase"
lote= "contains introns"
                                                                         ocation/Qualifiers
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/number= 3
5542. .5654
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                                                                                          promoter
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Escherichia coli.
Zea mays.
Agrobacterium tumefaciens.
Synthetic.
Chimeric.
                                                                                                                                                     misc_feature
                                                                                                       3'UTR
                                                                                                                      3'UTR
                                                                     exon
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Peroxidase; per5 gene; maize; corn; transgenic plant; promoter; root; vector; plasmid PerGUS16; beta-glucuronidase; uidA; reporter gene; ds; circular; cyclic.
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Location/Qualifiers promoter

rtag= a note= "per5 promoter and untranslated leader" "per5 exon 1" .4263 note=

t= "beta-glucuronidase" ." "Escherichia coli uidA reporter gene" lote=

"3' untranslated region from pBI221" .6396 note=

= e = "nos 3'UTR" .6407 note= "linker" 408. .9299 misc\_feature

\*tag= g note= "Bluescript II SK-" WO9856921-A1

17-DEC-1998

98WO-US011921. 10-JUN-1998;

12-JUN-1997;

(DOWC ) DOW AGROSCIENCES LLC

Folkerts O, Hopkins N, Menke MA; Woosley A; Belmar S, Smith K, Armstrong K, Petolino JF, Ainley M, Pareddy D,

NPI; 1999-080904/07.

New isolated regulatory sequences for transgenic plants - which are derived from the malze root preferential cationic peroxidase protein (per5) gene

Example 11; Page 108-112; 150pp; English

This is the nucleotide sequence of PerGUS, a plasmid containing 4 kb of the maize root preferential cationic peroxidase per5 gene comprising the per5 promoter, untranslated leader, and the first 5 codons of the coding region (1.e. nucleotides 1-4200 of the sequence given in AAV63717), as well as the GUS gene, and the nos 3' untranslated region (3'UTR). It does not include an intron in the untranslated region. The invention relates to new isolated regulatory sequences, especially promoter, intron and 3'UTR sequences, of the maize per5 gene. Claimed recombinant gene cassettes comprising per5 regulatory sequences are used to control expression of recombinant genes in selected tissue, especially the root, of transformed plants, particularly maize

Sequence 9299 BP; 2573 A; 2114 C; 2158 G; 2453 T; 0 U; 1 Other;

ö 0; Indels '0; Gaps Query Match 3.9%; Score 32; DB 2; Length 9299; Best Local Similarity 100.0%; Pred. No. 4.9e-06; Matches 32; Conservative 0, Mismatches 0; Indels

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5, 2006, 11:35:52 completed: March ne : 560 secs Search con Job time ug-10-660-208-90.olig.rge

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Submitted (03-FBB-2005) Broad Institute of MIT and Harvard, 320 Charles Street, Cambridge, MA 02141, USA
101 CATTCAATAAATTAAAGTGACCAATCAGATAGTCTC 136
                                                                                                                                                                                                                                                                                                                     clone ZMMBBb0309E13
                                                                                                                                                                                                                                                                                                                           Zea mays, clone ZMMBB
Unpublished
2 (bases 1 to 69497)
                                                                                                                                                                                                                                                                                                           and Messing, J.
                                                                                                                                                     ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                             RESULT 14
AC149816/c
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JOURNAL
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JOURNAL
                                                                                                                        DEFINITION
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AUTHORS
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JOURNAL
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KIRGDVDTVTVVVRADAGRSGKSLANEMKVGYVESAGSSPAKTDLAELAALLAKNLVD
ETAAVAAFQGDVLVYGGANLTLVDWEQVDLYGLEIKGQRPVHVEYGWDGVGDEGAVLV
OPDADGRGRLVTAVLPGDEIDSLRAALGSALQVA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NDCGVRIVEARCDRDWAEWIRDAAPGRIRQLCYDKVLGPELFFSFLLYVQITNFKCGG
LALGESWAHLIGDIPSAATCFNKWAQILSGKKPEATVLTPPNQPLOGGSPAAFRSVKQ
                                                                                                                                                                                                                                                                                                                                                                                         Tacke, E., Korfhage, C.; Michel, D., Maddaloni, M., Motto, M.,
Lanzini, S., Salamini, F. and Doring, H.P.
Transposon tagging of the maize Glossy2 locus with the transposable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHYLRGVYYYRSGDGLATKVLKDPMLPWLDDHFPVAGRVRRAETEGDGAPRRPYIKC
                                                                                                                                                                                                                         PLN 09-MAY-1996
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                                                                                                                                                                                                                                                                                                                        Zea mays
Sukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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Submitted (19-UUN-1995) E. Tacke, Max-Planck-Institute, Dept.
Salamini, Carl-von-Linne-Weg 10, 50829 Koeln, NRW, FRG
                                                                                    Gaps
                                                     Length 198102;
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                                                                                  0; Indels
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                                                                                                                92 CAAICAGAACATICAATAAATTAAAGIGACCAAICAG 128
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Pred. No. 1.6e-09;
0; Mismatches 0;
                                                    Score 37; DB 14; L
Pred, No. 4.9e-10;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               xref="UniProt/TrEMBL:Q41809"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organisme="Zea mays"
/mol_type="genomic DNA"
/mol_type="genomic DNA"
/db xref="tea.taxon:457"
/clone lib="EMBL4/Sau3A"
/note="Glossy2 locus; Gl2"
join(1979. 2607,3924. 5001)
/number=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              oin(2152. .2607,3924. .4748)
gene="orf"
                                                                                                                                                                                                                            DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein_id="CAA61258.1"
db_xref="GI:949980"
                                                                                                                                                                                                                            6343 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                             element En/Spm
Plant J. 8 (6), 907-917 (1995)
              /estimated_length=100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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100.0%; Pref
                                                                                                                                                                                                                            Z.mays Glossy2 locus DNA.
                                                     4.5%; Sco
Local Similarity 100.0%; Pr
hes '37; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      codon start=1
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/gene="orf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 6343)
                                                                                                                                                                                                                                                                          X88779.1 GI:949979
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Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acke, E.
                                                                                                                                                                                                                                                                                                           Zea mays
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                                                            Query Match
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                                                                                                                                                                                                                            LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                            Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
PUBMED
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA.
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                                                                                                                                                                                               RESULT 13
ZMGLOSSY
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Siren, B., Nusbauum, C., Lander, E., Butler, E., Wing, R., Bharti, A.K., Messing, J., Abouelleil, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslarkiy, L., Arachchi, H.M., Barna, J., Chang, J., Choepel, Y., Collymore, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., PitzGerald, M., Gage, D., Galegan, J., Farco, S., Ferrelara, P., FitzGerald, M., Gage, D., Galegan, J., Gardyna, S., Graham, L., FitzGerald, M., Gage, D., Galegan, J., Hagopian, D., Hagos, B., Hall, J., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, G., Kamat, A., Karates, A., Kells, C., Landers, T., Levino, R., Linchlad, Toh, K., Liu, A., Mabbit, R., Wactean, C., Macdonald, P., Ilu, G., Liu, X., Lui, A., Mabbit, R., Maches, C., Macdonald, P., Major, J., Mathews, C., McCarthy, M., Meldrim, J., Melenga, L., Micol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Nell, D., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Nell, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Spencer, B., Stange-Thomann, N., Stojanovic, N., Travers, M., Wasillev, H., Venkataraman, V. S., Viell, R., Volan, Whison, B., Wu, X., Wasillev, H., Venkataraman, V. S., Viell, R., Volan, Whann, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission
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AL Submitted (12-UN-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
Research, 320 Charles Street, Cambridge, MA 02141, USA
Research, 320 Charles Janeet, Cambridge, MA 02141, USA
Shiren, B., Nusbaum, C., Lander, E., Butler, E., Wing, R., Bharti, A.K., Messing, J., Abouelleil, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguelavkiy, L., Arachchi, H.M., Barna, M., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Farc, S., Ferreira P., Gook, A., Cooke, P., Corum, D., Hagopian, D., Hagos, B., Hall, J., Granders, M., Hafez, N., Hadez, M., Hall, J., Harten, M., Hafez, N., Hadopian, D., Hagos, B., Hall, J., Harten, M., Lilevi, T., Johnson, R., Jones, C., Kamat, A., Lui, A., Mabbitt, R., Maclean, C., Macdonald, P., Manning, J., Mathews, C., Maccenthy, M., Meldrim, J., Manning, J., Mathews, C., McCarthy, M., Meldrim, J., Norbu, C., Maylor, J., Nguyen, C., Nachi, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Vaning, R., Seury, P., Smith, C., Spencer, B., Stange-Thomann, N., Stohban, K., Travers, M., Tangers, M., Tangers, M., Tangers, M., Tangers, M., Tangers, M., Tangers, M., Vasatlas, J., Tesfaye, S., Theodore, J., Tophan, K., Travers, M., Mann, D., Veine, G. Zainenn, J. Zembak, L., Zaimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                        AC149816 69497 bp DNA linear HTG 03-FEB-2005
Zea mays clone ZMMBBb0309El3, *** SEQUENCING IN PROGRESS ***, 7
unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta; Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoldeae, Andropogoneae, Zea.

1 (Deses 1 to-69497)
Birren, B., Nusbaum, C., Lander, B., Butler, B., Wing, R., Bharti, A.K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC149816
AC149816.2 GI:57790137
HTG: HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
Zea maye
3715 CATTCAATAAATTAAAGTGACCAATCAGATAGTCTC 3750
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10-OCT-2000 (first entry)

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New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for
plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
                              extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield; protein content; gene; se.
                                                                                                                                                                                                                                                                                                  Tabaska JE,
                                                                                                                                                                                                                                                                                                  Screen SE,
                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 22826; 15pp; English.
                                                                                                                                                               28-APR-2003; 2003US-00425114;
                                                                                                                                                                                    06-MAY-1999; 99US-00304517, 05-NOV-2001; 2001US-00985678.
                                                                                                                                                                                                                                                                                                  Kovalic DK,
                                                                                                                                                                                                                                                                                                                       WPI; 2004-180133/17.
                                                                                                                                                                                                                                        KOVALIC D K.
                                                                                                                                                                                                                                                                 TABASKA J E
                                                                                                                                                                                                                                                     SCREEN S E.
                                                                                                                     US2004034888-A1
                                                                                                                                                                                                                                                                                                 Zhou Y,
                                                                                                                                                                                                                                                                                                                                                                            improving yield
                                                                                                                                                                                                                                ZHOU Y
                                                                                                                                                                                                                       LIU J.
                                                                                                                                                                                                                                                                            CAO Y.
                                                                                                Unidentified.
                                                                                                                                           19-FEB-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention
                                                                                                                                                                                                                                                                (TABA/)
                                                                                                                                                                                                                     (LIUJ/)
(ZHOU/)
                                                                                                                                                                                                                                          (KOVA/)
(SCRE/)
                                                                                                                                                                                                                                                                                                  Liu J,
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The invention describes a recombinant DNA construct comprising a polynuclectide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at the savilable in electronic form from the US patent office at the savilable of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, lignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert
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                                  4.4%; Score 36; DB 13; Length 1578; 100.0%; Pred. No. 3.6e-08; ive. 0; Mismatches 0; Indels
Sequence 1578 BP; 380 A; 391 C; 429 G; 378 T; 0 U; 0 Other;
                                                                           36; Conservative.
                                      Query Match
Best Local Similarity
Matches 36; Conserv
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· 148 ATAGAGCTAAGACACTGTGTCTTCGTCAAGATACAT 183
                                                                         Aradadctaadacactercricercaadaracar 873
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AAAS7891 standard; DNA; 6343 BP
                                    AAA57891;
AAA57891
ID AAA!
XX: AAA!
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RESULT 13

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The invention relates to transforming a plant cell with either a nucleic acid encoding a plant cuticular lipid biosynthetic protein, or an antisense nucleic acid sequence targetted to a plant cuticular lipid gene, and then generating a plant from the plant cell. The cuticular lipid genes that may be used in the invention are given in AAA57811-A57884 and AAA57891. The cuticular centeristic polymerised hydroxy-fatry acids embedded in a complex mixture of nompolar lipids (the cuticular wax). The cuticle protects and strengthens the plants, prevents evaporation of internal fluids and filters UV radiation. Mutations in the cuticular lipid genes affects the clustic and composition of cuticular lipids; in maize, 17 loci (the glossy (gl) genes) have been identified as being in involved in cuticular lipid biosynthesis or control. The method is useful for introducing a nucleic acid into a cell preferably of maize, soybean, rapessed, canola, cotton, safflower, peanut, palm or sunflower plant and generating a plant from the plant cell. The transformed plants have improved environmental from the plant cell. The transformed plants have improved environmental from the plant cell. The transformed plants have improved environmental from the plant cell. The transformed plants have improved environmental crommental control.
                                                                                               Maize, glossy2; gl2; cuticle; cuticular lipid biosynthesis;
lipid composition; lipid quantity; disease resistance; pest resistance;
wind resistance; frost resistance; UV resistance; transgenic plant;
antisense inhibition; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transforming plants such as maize and canola, for producing new plant varieties having disease and pest resistance involves introducing cuticular lipid genes into the plant genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seeds. The present sequence represents the maize glossy2 (gl2) gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6343 BP; 1493 A; 1667 C; 1607 G; 1564 T; 0 U; 12 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 6343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Robertson DS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               viral disease resistance, pest resistance, and altered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maize per5 root preferential cationic peroxidase gene.
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Pred. No. 3.7e-08;
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4.4*; Score 36; DB
Best Local Similarity 100.0*; Pred. No. 3.7
Matches 36; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       (IOWA ) UNIV IOWA STATE RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 7; Col 115-122; 69pp; English
                                                                                                                                                                                                                                                                                                                                                               95US-00581148.
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                                                           Maize glossy2 (gl2) gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-349707/30.
                                                                                                                                                                                                                                                                                                                                                               29-DEC-1995;
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WPI; 1999-080904/07.
P-PSDB; AAW87893.
                                                                                                                                                                                                                                          10-JUN-1998;
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                                                                                                                                                                                   WO9856921-A1
                                                                                                                                                                                                               17-DEC-1998.
                                                                                                                                                                                                                                                                                                                            Ainley M, A
Pareddy D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                             (per5) gene.
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AAV63730
                                                                      exon
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Peroxidase; per5 gene; maize; corn; transgenic plant; promoter; root; ds
                                                                                                                                                                                                                                                      1532. 4148
*tag= d
note= "this region is specifically claimed in Claim 1"
187. 4215
*tag= i
                                                                    . .4215
*tag= a
note= "this region is specifically claimed in Claim 1"
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201. .6068
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383. .5548
                                                                                                                           *tag= c
note= "this region is specifically claimed in Claim 1"
                                                                                                                                                                                                                            note = "this region is specifically claimed in Claim 1"
                                                                                                                                                                                                                                                                                                                                                       note= "this region is specifically claimed in Claim 1" 187. .4200
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note= "this region is specifically claimed in Claim 1"
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5250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "contains introns"
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                                                       ocation/Qualifiers
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/number= 3
5542. .5654
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/*tag= r
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note= '
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This is the nucleotide sequence of the maize pers root preferential cationic peroxidase gens, which encodes a 33-amino acid peroxidase cationic peroxidase gens, which encodes a 33-amino acid peroxidase cationic polypeptide (see AAW87893). Genomic clones comprising pers sequences were isolated from a maize W12 genomic library using a probe based on isolated pers cont. Overlapping subfragments of the gene were sequenced to certain the complete 6550 bp sequence of the pers gene. Regulatory content to the complete 6550 bp sequence of the pers gene. Regulatory contents for controlling expression of recombinant gene cassettes for controlling expression of recombinant gene is specially the root, of transformed plants, particularly maize. The gene cassettes can be used for expression of heterologus genes such as those that confer tolerance to harbicides, insects or viruses, and genes that provide improved nutritional value or processing characteristics to the plant. Use of the pers 3'UTR sequences provides characteristics to the plant. Use of the pers 3'UTR sequences provides 3'UTR.
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sequence is specifically claimed in Claim 2"
                                                                                                                                                                                                                                                                                       /*tag= y
/note= "transcription termination sequence, specifically
claimed in Claim 3"
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/numbe== 3
/note= "this intron is specifically claimed in Claim 2"
5650. .6065
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100.0%; Pred. No. 4.9e-06;
tive 0; Mismatches 0;
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Woosley A;
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Smith K,
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Petolino JF,
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Peroxidase; per5 gene; maize; corn; transgenic plant; promoter; root; vector; plasmid PerGUS16; beta-glucuronidase; uidA; reporter gene; ds; circular; cyclic.
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Zea mays. Agrobacterium tumefaciens. Synthetic. Chimeric. Escherichia coli

"per5 promoter and untranslated leader" Location/Qualifiers 48. .4247 prómoter exon

t= "beta-glucuronidase" "Escherichia coli uidA reporter gene" "per5 exon 1" note= 3'UTR

note= "3' untranslated region from pBI221"

.6396 tag= 3' UTR

"nos 3'UTR" "linker" note≃ \*tag≃ 3397 misc\_feature misc\_feature

/\*tag= g /note= "Bluescript II SK-' WO9856921-A1

.7-DEC-1998

98WO-US011921. 10-JUN-1998;

12-JUN-1997;

DOWC ) DOW AGROSCIENCES LLC.

Menke MA; Folkerts O, Hopkins N, Woosley A; Belmar S, Smith K, Armstrong K, Petolino JF, Ainley M, Pareddy D,

WPI; 1999-080904/07

New isolated regulatory sequences for transgenic plants - which are derived from the maize root preferential cationic peroxidase protein per5) gene

Example 11; Page 108-112; 150pp; English

This is the nucleotide sequence of PerGUS, a plasmid containing 4 kb of the maize root preferential cationic peroxidase per5 gene comprising the per5 promoter, untranslated leader, and the first 5 codons of the coding region (i.e. nucleotides 1-4200 of the sequence given in AAV63717), as well as the GUS gene, and the nos 3' untranslated region (3'UTR). It does not include an intron in the untranslated region. The invention relates not include an intron in the untranslated region. The invention relates 3'UTR sequences, of the maize per5 gene claimed recombinant gene cassettes comprising per5 regulatory sequences are used to control expression of recombinant genes in selected tissue, especially the root, transformed plants, particularly maize

Sequence 9299 BP; 2573 A; 2114 C; 2158 G; 2453 T; 0 U; 1 Other;

Query Match 3.9%; Score 32; DB 2; Length 9299; Best Local Similarity 100.0%; Pred. No. 4.9e-06; Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps

1462 TCTAAAACATGTGTCTTACCATATTCATTGTA 1493 59 TCTAAAACAIGIGICTTACCATATTCATIGTA 90 à 셤

5, 2006, 11:35:52 completed: March Search co

34         4.1 117844         14 ACISS360         ACISS367 Zee maye           34         4.1 170318         14 ACISS367         ACI49615         Zee maye           34         4.1 18996         14 ACI48153         ACI49630         Zee maye           33         4.0 116794         14 ACI48152         Zee maye           33         4.0 187674         14 ACI49640         ACI49630         Zee maye           32         3.9 6550         6 ARA82064         BD13269         ACI49640         Zee maye           32         3.9 6550         6 ARA82064         BD132705         ARA82060         Sequence           32         3.9 6550         6 ARA82070         ARA82070         Sequence           32         3.9 6550         6 ARA82070         ARA82070         Sequence           32         3.9 6550         6 ARA82070         ARA82070         Sequence           32         3.9 9408         6 ARA20900         ARA82070         Sequence           32         3.9 9408         6 ARA82070         ARA82070         Sequence           32         3.9 9408         6 ARA20900         ARA82070         Sequence           32         3.9 9408         6 ARA82070         ARA82070         Sequence		Conner,T.W., Dubois,P. Plant regulatory seque Patent: WO 0183709 LL Monsanto Technology LL Location/Qual 1. 813 /organism="ze/mol_type="un/db_xref="tax"	Local Similarity 100.0%; Score 823; DB 6; Length 823; Local Similarity 100.0%; Pred. No. 0; Length 823; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0; CTGCACGGTACTCCAAGTATAAGACACACATAATGCAGTAGTAGTGC 60 1 CTGCACGGTACTCCAAGTATAAGACACACACATAATGCAGTAGTGCATGTC 60 9: TAAAACATGTGTTACCATATTCATTGTATCAATCAGAACATTAAAATTAAAGTG 120 1: TAAAACATGTGTTTACCATATTGTATGAATCAGAACATTCAATAAATTAAAGTG 120 1: TAAAACATGTGTTTACCATTGTATGTATGAATCAGAACATTCAATAAATTAAAGTG 120 1: TAAAACATGTGTTTACCATTGTATGTATGAATCAGAACATTCGTCAAGATA 180 1: CCAATCAGATAAATTAAAGACATTCGTCAAGATA 180 1: CCAATCAGATAAATTAAAGACATCACACACTGTGTGTTTTACATTAACATTCAAGACATTAAGAC 240 1: CAATCAGATTAATAACATTCACCCCCTAGACACACTCAAGATA 180 1: CAATCAGATTAATAACATTCACCCCCTAGACACACTCAAGATA 180 1: CAATCAGATTAATAACATTCACCCCCTAGACACACTCAAGACATAAAGAC 240 1: CAATCAGATTAAAGAC 240 1: CAATCAGATTAAAGAC 240 1: CAATCAGATTAATCATTCACCCCCTAGACACACTCAAGACATTAAGAC 240 1: CAATCAGATTAATCACTCCTCAAGACACACTCTAAGACACATTAAGAC 240 1: CAATCAGATTAATCACTCCTCAAGACACTCTAAGACCATTAAGAC 240 1: CAATCAGATTAATCACTCCTCTAGACACACTCTAAGACACTTAAGAC 240 1: CAATCAGATTAATCACTCCTCTAGACACACTCTAAGACCACTTAAGAC 240 1: CAATCAGATTAATCACTCCTCTAGACACACTCTAAAGACCATTAAGAC 240 1: CAATCAGATAAATTAACCCCTCTAGACACACTCTAAACACTCTTAAGAC 240 1: CAATCAGATAAATTAACACCCCTCTAGACACACTCTAAACACTCTTAAGAC 240 1: CAATCAGATAAAACACTCTTAAACACTCTTAAACACTCTTAAACACTCTTAAACACACTCTAAACACACTCTAAACACACTCTAAAACACACTCTAAACACACTCTAAACACACTCTAAACACACTCTAAAACACACTCTAAAAACACACTCTAAAAACAAC
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GenCore version 5.1.7  Copyright (c) 1993 - 2006 Biocceleration Ltd.  OM nucleic - nucleic search, using sw model  Run on: March 5, 2006, 11:18:36; Search time 4262 Seconds (without alignments)  Title: US-10-660-208-90  Perfect score: 823 Sequence: 1 ctgcacggtactccaagtatcgatccattctccagcgcag 823 Scoring table Search of Gapex 60.0  Searched: 5883141 seqs, 28421725653 residues  Morchistzentiment of hits satisfying chosen parameters: 11766282  Minimum DB seq length: 0  Maximum DB seq length: 2000000000  Post-processing: Listing first 45 summaries	Database: GenEmbl:*  1: gb_ba:* 2: gb_in:* 3: gb_env:* 4: gb_on:* 5: gb_ov:* 6: gb_pat:* 7: gb_ph:* 10: gb_ba:* 11: gb_v:* 12: gb_un:* 13: gb_un:* 11: gb_v:* 12: gb_un:* 13: gb_vi:* 14: gb_vi:* 15: gb_vi:*	Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being I and is derived by analysis of the total score distribution.  SUMMARIES  Query  Score Match Length DB ID  Score Match Length DB ID  Score Match Length DB ID  Score Match Length DB ID  Score Match Length DB ID	1587 6 AX29946 AX29946 AX29946 B 149882 14 AC155395 AC15598 AC15598 AC15598 AC15598 B 182004 14 AC155608 Continual B 18326 14 AC155578 AC155578 AC155578 AC155578 AC155578 AC155578 AC155578 AC149836 AC149836 AC149836 AC149836 AC149836 AC149836 AC149836 AC149836 AC149836 AC149836 AC149836 AC149836 AC149836 AC149836 AC14589 AC149836 AC149836 AC149836 AC149836 AC149836 AC149836 AC1498379 AC149816 AC149836 AC149836 AC149836 AC149836 AC149836 AC1498379 AC149816 AC149836 AC149836 AC149836 AC149816 AC151050 AC

1390

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149882 bp DNA linear HTG 25-JAN-2005
Zea mays strain B73 clone ZMWBBb0160F12, *** SEQUENCING IN PROGRESS
***, 13 unordered pieces.
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Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H., Chterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M., Schubert, K., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T., Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and Quackenbush, J.
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                                                                                                                                                                                                                      Genomic Research (TIGR)
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CAGAAGTATTGTGGCTGCATATTGCTGAAATTATAGCGAGGGCCCAAGGCCCATCACTTC
                                            TAAGCAAACAAGCGAACATTGCTTAGCTACAACCAATTTGCTGGGCTTCCATGGGCATCG
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Plant regulatory sequences for selective control of gene expression
Patent: WO 0183790-A 87 08-NOV-2001;
Monsanto Technology LLC (US)
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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/mol_type="unassigned |
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AX299946
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                                     Web site: http://www.tigr.org/tdb/tgi/maize/
Contact: maize@tigr.org
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Length 149882;

DB 14;

12.5%; Score 103;

Query Match

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51039 CGAATATAGAGCTAAGACACTGTGTCTTCGTCAAGATACATGTCTTGAGATTTTTTTACAT 50980
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Zea mays strain B73 clone ZMMBBC0261N01, *** SEQUENCING IN PROGRESS
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Chan, A.P., Pertea, G., Zheng, L., Cheung, P., Lee, D., Koo, H.,
Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M.,
Schubert, K., SanMiguel, P., Ma, J., Pontearoli, A.C., Rohlfing, T.,
Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and
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Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M.,
Schubert, K., Sanwiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T.,
Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and
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2104: gap of unknown length
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15240: gap of unknown length
16541: contig of 1301 bp in length
16641: gap of unknown length
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Pred. No. 1.3e-50; Mismatches 0;
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21677
24624
24724
28117
28217
29535
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43862
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match

9.2%; Score 76; DB 14; Length 18
Best Local Similarity 100.0%; Pred. No. 5.3e-34;
Matches 76; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                          /estimated length=unknown
112665. 112764
/estimated length=unknown
122910. 123009
/estimated length=unknown
127131. 127230
                                                                                                                                                                                                              /estimated length-unknown 67581. 67680
/estimated length-unknown 68777. 68876
/estimated length-unknown 88494. 85593
/estimated length-unknown 96198. 90518.
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130720. 130819
/estimated length=unknown
140094. 140193
/estimated length=unknown
162844. 152943
/estimated length=unknown
167187. 167286
                                    /estimated length-unknown
40513. 40612
/estimated length-unknown
43862. 43361
/estimated length-unknown
48430. 48529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              estimated length=unknown 77306. .177405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       estimated length=unknown 69931. 170030 estimated length=unknown 75432. 175531
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                                                                                                                                                    /estimated length=unknown 50890. .60989 /estimated length=unknown 55148. .65247
9535. .zvo.v
estimated length=unknown
12649. .32748
                                                                                                                          estimated length=unknown 9230. .59329
                                                                                                                                                                                                                                                                                                                                     estimated length=unknown 11501. .111600
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110000
210000
310000
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AY664417 1/C
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Fragment Name
AY664417 0
AY664417 1 10
AY664417 2 20
AX664417 3 30
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ig of 8086 bp in length of unknown length of g of 9184 bp in ''
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of 5369 bp in length
unknown length
of 10782 bp in length
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bp in length
length
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193326: contig of 13541 bp in length
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bp in length
length
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of 13523 bp in length
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gap of unknown length
contig of 13523 bp in length
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175778: contig of 2277 bp in length
                           unknown length
of 8374 bp in length
                                                                                                                                          of 4765 bp in length
                                                                                                                                                           unknown length
of 4799 bp in length
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of 7785 bp in length
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of 9714 bp in length
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of 3896 bp in length
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/estimated length=unknown
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/strain="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:4577"
/clone="ZMMBBc0190D10"
2169. .2268
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55708:
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86786:
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331292
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Continuation (2 of 4) of AY664417 from base 100001 (AY664417 Zea mays cultivar Mol7 locu
                                                                                                                193326 bp DNA linear HTG 25-JAN-2005
Zea mays strain B73 clone ZMWBBc0190D10, *** SEQUENCING IN PROGRESS
***, 34 unordered pieces.
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3 (bases 1 to 193326)
Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H., Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M., Schubert, K., SanMiguel, P., Ma, J., Pontaroli, A.C., Robling, T., Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and Quackenbush, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (25-JAN-2005) The Institute for Genomic Research (TIGR),
9712 Medical Center Dr. Rockville, MD 20850
On Jan 25, 2005 this sequence version replaced gi:57863099.
                                                                                             173 TCAAGATACATGTCTTGAGATTTTTTACATTCACCCCCTAGACACACTCTAAGACACAA 232
                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H., Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M., Schubert, K., Sanmiquel, P., Ma, J., Pontaroli, A.C., Rohlfing, T., Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and Quackenbush, J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Consortium for Maize Genomics - BAC skim sequencing and assembly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 34 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                             ·,
                                Length 110000;
                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www.tigr.org/tdb/tgi/maize/
Contact: maize@tigr.org
                             Query Match
8.9%; Score 73; DB 15; I
Best Local Similarity 100.0%; Pred. No. 3.6e-32;
Matches 73; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                Spermatophyta; Magnoliophyta; Lilio
clade; Panicoideae; Andropogoneae;
                                                                                                                                                                                                                                                                                                                                            AC155578.2 GI:58082437
HTG; HTGS_PHASE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 193326)
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Seq_lib_id: ZGES
                                                                                                                                                                                    CTTAAGACACCCA 88387
                                                                                                                                                              233 CTTAAGACACCCA 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                  Zea mays
                                                                                                                                                                                             88399
                                                                                                                                                                                                                                                                                                                                              VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
JOURNAL
REFERENCE
AUTHORS
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AUTHORS
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JOURNAL
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AC155578
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148120 bp DNA linear HTG 25-JAN-2005 Zea mays strain B73 clone ZMMBBC0062P13, *** SEQUENCING IN PROGRESS AC155517
                                                                                                                                                                                                                                                                         Eukaryophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for Genomic Research (TIGR),
20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (15-JAN-2005) The Institute for Genomic Research (TIGR), 9712 Medical Center Dr, Rockville, MD 20850
3 (bases 1 to 148120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
( base)
( base)
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( chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H.,
Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H.,
Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M.,
Schubert, K., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T.,
Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and
                                                                                                                                                                                                                                                                                                                                    Chan, A.P., Pertea, G., Zheng, L., Cheung, P., Lee, D., Koo, H., Leterback, T.R., Peldblyum, T.V., Rabinowicz, P., Fraser, C.M., Schubert, K., Sanwiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T., Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and Quackenbush, J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Consortium for Maize Genomics - BAC skim sequencing and assembly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (25-JAN-2005) The Institute for Genomic Research 9712 Medical Conter Dr. Rockville, MD 20850 on Jan 25, 2005 this sequence version replaced gi:57863038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 15 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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gap of unknown length
contig of 30354 bp in length
contig of 1983 bp in length
contig of 1983 bp in length
contig of 1983 bp in length
contig of 15404 bp in length
contig of 15404 bp in length
contig of 18404 bp in length
contig of 1841 bp in length
contig of 18109 bp in length
contig of 18109 bp in length
contig of unknown length
gap of unknown length
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                                                                                                                                                                                                     GI:58082377
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38265:
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Seq_lib_id: ZOBH
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HTG; HTGS_PHASE1.
Zea mays
Zea mays
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100.0%; Pred. No. 8.8e-25;
tive 0; Mismatches 0;
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40476 40575
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estimated length=unknown
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18464. .1<u>1</u>8563
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74476. .74575
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CGAATATAGAGCTAAGACACTGTGTGTCTTCGTCAAGATACATGTCTTGAGATTTTTTACAT 202

61; Conservative

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Gaps

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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopaida, Poalea, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.

., Nusbaum, C., Lander, E., Butler, E., Wing, R., Bharti, A.K.

Lander, E.,

2 (bases 1 to 112468) Birren, B., Nusbaum, C.,

TITLE JOURNAL REFERENCE AUTHORS

clone ZMMBBc0496L17

1 (bases 1 to 112468) Birren, B., Nusbaum, C.,

REFERENCE AUTHORS

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16123 bp in length
                                                                                                                                                            contig of 13569 bp in length
gap of unknown length
contig of 3600 bp in length.
                                                                             of 18267 bp in length
unknown length
                unknown length
of 3360 bp in length
unknown length
of 3502 bp in length
                                                                                                         of 1181 bp in length
unknown length
of 5072 bp in length
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5e-18;
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|estimated_length=unknown
98870. 98859
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174799. .124398
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1694. .61793
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clone="ZMMBBc0062P13"
                                                                                                                                                                                                                              organism="Zea mays"
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REFERENCE AUTHORS

Messing, J., Abouelleil, A., Allein, N., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Buckhi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Bouckhalter, B., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Cook, A., Cocve, P., Galagan, J., Gardyna, S., Graham, L., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, K., Marlis, C., McCarthy, M., Maldrim, J., Maning, J., Matthews, C., McCarthy, M., Maldrim, J., Maning, J., Matthews, C., McCarthy, M., Maldrim, J., Nicol, R., Dui, A., Mangas, V., Murphy, T., Nicol, R., Deterson, K., Phunkhang, P., Plerre, N., Nicol, R., Deterson, K., Phunkhang, P., Plerre, N., Schupez, J., Schupez, S., Schupez, S., Schupez, S., Schupez, S., Stuppac, J., Topham, K., Travers, M., Vassille, W., Vorkatzaraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wasille, H., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission

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Bharti, AK and Messing, J: The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers, The State University of New Jersey, 190 Frealinghuysen Road, Piscataway, NJ 08854, USA (http://pgir.rutgers.edu)
Butler, E and Wing, R: Arizona Genomics Institute, Biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vassillev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X
Wyman, D., Young, G., Zalnoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (03-FBB-2005) Broad Institute of MIT and Harvard, 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Charles Street, Cambridge, MA 02141, USA
On Jan 14, 2005 this sequence version replaced gi:49035067,
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://frp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: sequence submissions@broad.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Broad Institute of MIT and Harvard
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Web site: http://www-seg.wi.mit.edu
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Direct Submission
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Zea mays clone ZMMBBC0496L17, *** SEQUENCING IN PROGRESS ***,
ordered pieces.
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HTG; HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN.
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Zea mays Zea mays

ACCESSION VERSION · KEYWORDS SOURCE ORGANISM

RESULT 8 AC149836 LOCUS DEFINITION

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78584: 9
99756: 0
99856: 0
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
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                                                                                                                                                                                                    * NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced

by the finished sequence as soon as it is available and the accession number will be preserved.

the accession number will be preserved.

$ 52778 contig of $6277 bp in length $ 62778 contig of $49691 bp in length.
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Phunkhang, P., Pierre, N.,
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HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 5.6%; Score 46; DB 14; I
Best Local Similarity 100.0%; Pred. No. 1.4e-15;
Matches 46; Conservative 0; Mismatches 0;
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Unpublished
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/organism="Zea mays"
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Ulrect Submitsblon

Numberd (12-JUN-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
Research, 320 Charles Street, Cambridge, MA 02141, USA
Research, 320 Charles Street, Cambridge, MA 02141, USA

1 (Dases 1 to 143793)
RS Birran,B. Nusbann,C., Lander,E., Ming,R., Bharti,A.K., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Arachchi,H.M., Barna,N., Chang,J., Choepel,Y., Collymore,A., Cooke,P., Corum,B., DeArellano,K., Diaz,J.S., Dodge,S., FitzGerald,M., Gage,D., Chang,J., Choepel,Y., Collymore,A., FitzGerald,M., Gage,D., Galagan,J., Farco,S., Ferreita,P., FitzGerald,M., Gage,D., Hagos,B., Hall,J., Grand-Pierre,N., Hafez,N., Halloy, Hagoplan,D., Hagos,B., Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Johnson,R., Machen,C., Kamat,A., Kallade,C., Landers,T., Levine,R., Lindblad-Toh,K., Lui,A., Mabbitt,R., Machen,C., Machen,C., Machen,C., Machen,C., Machen,C., Machen,C., Machen,C., Machen,C., Machen,C., Machen,C., Machen,C., Machen,C., Machen,C., Machen,C., Machen,C., Machen,C., Machen,C., Machen,C., Norbu,C., O'Connor,T., O'Donnell,P., O'Donnell,P., O'Norbu,C., O'Connor,T., O'Donnell,P., Schuuer,S., Schuuer,S., Schuuer,S., Schuuer,S., Schuuer,S., Schuuer,S., Schuuer,S., Schuuer,S., Trevers,M., Travers,M., Tavers,M., Tav
                       Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,
Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travere, M.,
Vasailiev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X.,
Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bharti, AK and Messing, J: The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers, The State University of New Jersey, 190 Prelinghuysen Road, Piscataway, NJ 08854, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (03-FEB-2005) Broad Institute of MIT and Harvard, 320 Charles Street, Cambridge, MA 02141, USA On Jan 14, 2005 this sequence version replaced gi:49035053.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                * NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as truns of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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31007: gap of unknown length
36273: contig of 5266 bp in length
36373: gap of unknown length
45582: contig of 9209 bp in length
45682: gap of unknown length
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Contact: sequence_submissions@broad.mit.edu
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2ea mays strain B73 clone ZMMBBb0171P15, *** SEQUENCING IN PROGRESS
***, 3 unordered nieces
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H.,
Char, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H.,
Schubert, K., Sanhiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T.,
Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and
Quackenbush, J.
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Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M.,
Schubert, K., Sanwiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T.,
Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and
Quackenbuah, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Consortium for Maize Genomics - BAC skim sequencing and assembly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                  clone="ZMMBBC0051H21"
clone_lib="CHORI-201 Maize B73 BAC EcoRI Library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.6%; Score 46; DB 14; Length 143793; 100.0%; Pred. No. 1.4e-15; tive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29159 CTGCACGGTACTCCAAGTATAAGACACAGCTAAAACACACAACATAAT 29114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CTGCACGGTACTCCAAGTATAAGACACAGCTAAAACACAACATAAT 46
11 121040: gap of unknown length
11 123150: contig of 2110 bp in length
11 123250: gap of unknown length
11 143793: contig of 20543 bp in length.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ....... Project informaton
Web site: http://www.tigr.org/tdb/tgi/maize/
Contact: maize@tigr.org
                                                                                                                                                                                                                                                                                  ed_length=unknown
18584
                                                                                                                                                                                                                         /estimated_length=unknown
16274. .36373
estimated_length=unknown
15583. .45682
                                                                                                                                                                                                                                                                                                                                                                1 length=unknown
                                                                                                                                                                                                                                                                                                                                     estimated_length=unknown
                                                                                                                                                                                                                                                                                                                                                                                                             estimated length=unknown 23151. .123250
                                                                                                                                                                                                                                                                                                                                                                                                                                                 estimated_length=unknown
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                                                                                                                                                                                                          .31007
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Seq_lib_id: ZOED
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Best Local Similarity 100.0
Matches 46; Conservative
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                        121041
123151
123251
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AC166637/c
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PLN 18-APR-2005
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Clade; Panicoldeae; Andropogoneae; Zea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (09-JUN-1993) C.J. Staiger, John Innes Centre for Plant
Science Res., Dept. of Cell Biology, Colney Lane, Norwich NR4 7UH,
UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staiger, C.J., Goodbody, K.C., Hussey, P.J., Valenta, R., Drobak, B.K. and Lloyd, C.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
* NOTE: This is a 'working draft' sequence. It currently consists of 3 conties. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the conties are represented as * runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 4.9%; Score 40; DB 14; I
1 Similarity 100.0%; Pred. No. 6.9e-12;
40; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35921. .36020
/estimated length=unknown
80082. .80181
/estimated_length=unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Z.mays ZmPRO2 mRNA for profilin 2.
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/strain="inbred A188".
/db xref="taxon:4577"
/cell_type="pollen"
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Direct Summission

Submitted (01-JUL-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 198102)

S Birren, B., Nusbaum, C., Lander, E., Butler, E., Wing, R., Bharti, A.K., Arachchi, H.M., Barna, N., Allen, N., Anderson, M., Anderson, S., Arachchi, H.M., Barnata, J., Chong, J., Choepel, Y., Collymore, A., Cooke, P., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cooke, P., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cooke, P., Carum, B., Dakachlano, K., Diaz, J. S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., Fitzeerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hadfez, N., Hagopian, D., Hagos, B., Hall, J., Hulme, W., Illev, I., Johnson, R., Jindblad-Toh, K., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Mainhoy, J., Mathews, C., McCarthy, M., Meldrim, J., Meldrim, J., Meldrim, J., Meldrim, J., Nguyen, C.,
/translation="MSDRAKMSWQAYDEHLMCEIEGHHLAAAAIVGHDGAAWAQSTA
FPEFKTEDMANIMKDFDEFGHLAPTGLFLGPTKYMVIQGEFGAVIRGKKGSGGITVKK
TGQALVYGIYDEPMTFGQCNMVVERLGDYLLEQGM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC145389
20-JUN-2004
Zea mays clone ZMMBBC0054A01, *** SEQUENCING IN PROGRESS ***, 4
ordered pieces.
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Birren, B., Nusbaum, C., Lander, E., Butler, E., Wing, R., Bharti, A.K.
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                                                                                                                                                                                                                                                           Length 830;
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HTG; HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN.
                                                                                                                                                                                                                                                                                                                                                                                                 786 CCTCTCCCTCTCCGATCCATTCTCCAGCGCAG 823
                                                                                                                                                                                                                                                                                                                                                                                                                                   27 CCTCTCCCTCTCCCATCCATTCTCCCAGCGCAG 64
                                                                                                                                                                                                                                                                  DB 15; L
. 8.5e-11;
                                                                                                                                                              /note="2nd start codon; in-frame"
                                                                                                                                                                                                                                                              4.6%; Score 38; DB 100.0%; Pred. No. 8.5 iive 0; Mismatches
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Unpublished
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Best Local Similarity 100.C
Matches. 38; Conservative
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O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachopka, N., Ramasam, U., Raymond, C., Retta, R., Rise, C., No., Soman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Teffaye, S., Theodore, J., Topham, K., Traversh, W., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, C., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (Court of the court o
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* This sequence will be replaced

* by the finished sequence as soon as it is available and the accession number will be preserved.

* Dougle on number of 100 bp

* 20367 20366; gap of 100 bp

* 78635 78734; gap of 100 bp

* 78635 78734; gap of 100 bp

* 140319 198102: contig of 5184 bp in length

* 140419 198102: contig of 57684 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: sequence_submissions@broad.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
/cultivar="B73"
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140319. .140418
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101 CATTCAATAAATTAAAGTGACCAATCAGATAGTCTC 136
                                                                                                                                                  unordered pieces.
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                                                                                 RESULT 14
AC149816/c
                                                                                                                                                              ACCESSION
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AUTHORS
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                Tacke, E., Korfhage, C., Michel, D., Maddaloni, M., Motto, M.,
Lanzini, S., Salamini, F. and Doring, H.P.
Transposon tagging of the maize Glossy2 locus with the transposable
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                                                                                                                                                                                                                                 PLN 09-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KIRGDVDTVTVVVRADAAGRSGKSLANEMKVGYVESAGSSPAKTDLAELAALLAKNLVD
ETAAVAAFQGDVLVYGGANLTLVDMEQVDLYGLEIKGQRPVHVEYGMDGVGDEGAVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation="MVFEOHEEEAVAPGAVHGHRLSTVVPSSVTGEVDYALADADLAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VGPIEDLWLVPAGRDMACYSFHVSDAVLKKLHQQQNGRQDAAAGTFELVSALVWQAVA
                                                                                                                                                                                                                                                                                                                                     Spermatophyta; Tracheophyta; Embryophyta; Tracheophyta;
Clade; Panicoideae; Andropogoneae; Zea.
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Submitted (19-JUN-1995) E. Tacke, Max-Planck-Institute,
Salamini, Carl-von-Linne-Weg 10, 50829 Koeln, NRW, FRG
Location/Qualifiers
                                                  Length 198102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 4.4%; Score 36; DB 15; Length 6343; Best Local Similarity 100.0%; Pred. No. 1.6e-09; Matches 36; Conservative 0; Mismatches 0; Indels (
                                                                               0; Indels
                                                                                                                                                                                                                                linear
                                                                                                                                 173568 CAATCAGAACATTCAATAAATTAAAGTGACCAATCAG 173604
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                                                                                                            92 CAATCAGAACATTCAATAAATTAAAGTGACCAATCAG 128
                                                DB 14; L4.9e-10;
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db_xref="G1:949980"
db_xref="UniProt/TrEMBL:Q41809'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .6343

/organism="Zea mays"

/mol_type="genomic DNA"

/db xref="taxon:4577"

/clone lib="EMBL4/Sau3A"

/note="Glossy2 locus; Gl2"

join (1979. .2607,3924. .5001)
                                                                                                                                                                                                                                 DNA
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gene="orf"
join(2152, .2607,3924, .4748)
'gene="orf"
                                              4.5%; Score 37; DB 100.0%; Pred. No. 4.9 tive 0; Mismatches
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/estimated_length=100
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Plant J. 8 (6), 907-917 (1995)
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Z.mays Glossy2 locus DNA.
X88779
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3924. .5001
/number=2
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/gene="orf"
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                                                                             37; Conservative
                                            Query Match
Best Local Similarity
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ZMGLOSSY
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AUTHORS
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Sirren, B., Wingbaum, C., Lander, E., Wing, R., Bharti, A.K., Messing, J., Abouelleil, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Farco, S., Ferreira, P., Pitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand, P., Hagopian, D., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Illev, I., Johnson, R., Johnson, R., Johnson, R., Karatas, A., Kalls, C., Manchas, T., Lauders, T., Levine, R., Johnson, R., Macchanl, P., Major, J., Matchews, C., McCarthy, M., Meldrim, J., Manon, J., Matchews, C., McCarthy, M., Meldrim, J., Matchews, C., McCarthy, M., Meldrim, J., Marchy, T., Naylor, J., Nguyen, C., Wicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Klse, C., Rogov, P., Spencer, B., Stange-Thoman, N., Stojanovic, N., Stubbe, M., Valamas, J., Tesfaye, S., Theodore, J., Topham, K., Travere, M., Valamas, J., Tesfaye, S., Theodore, J., Topham, K., Travere, M., Waman, D., Young, G., Zannoun, V., Zembek, L., Zimmer, A. and Zody, M. Direct, Submission
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Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 69497)
Birren,B., Nusbaum,C., Lander,E., Butler,E., Wing,R., Bharti,A.K., Mesting,J., Abouelladi,A., Allen,N., Anderson,A., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y., Collymore,A., Cook,A., Cooke,P., Corum,B., DeArellano,K., Diaz,J.S., Dodge,S., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S., Graham,L., FritzGerald,M., Affez,N., Hagopian,D., Hagopian,L., Hallme,W., Lindela-Toh,K., Lindela-Toh,K., Lindela-Toh,K., Lindela-Toh,K., Lindela-Toh,K., Lindela-Toh,K., Lindela-Toh,K., Lindela-Toh,K., Lindela-Toh,M., Marbitt,R., Machen,C., Macdonald,P., Malory,J., Manning,J., Mathews,C., Maccathy,M., Major,J., Manning,J., Mathews,C., Moccathy,M., Major,J., Manning,J., Mathews,C., Moccathy,T., Naylor,J., Nguyen,T., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Pererson,K., Phunkhang,P., Plerre,N., Rachupka,A., Ramasamy,U., Reymond,C., Retta,R., Rese,C., Rogov,P., Roman,J., Schauber,S., Schupback,R., Seuery, P., Smith,C., Spencer,B., Stange-Thomann,N., Stohaba,K., Travers,M., Warman,D., Vonno,G., Zahnun, J., Zahmer, A., And P., Wilson,B., Wwman,D., Vonno,G., Zahnun,R., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M., Salmer,M.,
                                                                                                                                                                                                                                                                                                      bp DNA linear HTG 03-FEB-2005
, *** SEQUENCING IN PROGRESS ***, 7
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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ren,B., Nusbaum,C., Lander,E., Butler,E., Wing,R., Bharti,A.K.
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Submitted (03-FBB-2005) Broad Institute of MIT and Harvard, 320
Charles Street, Cambridge, MA 02141, USA
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3715 CATTCAATAATTAAAGTGACCAATCAGATAGTCTC 3750
                                                                                                                                                                                                                                                                                                      AC149816
Zea mays clone ZMMBBb0309E13,
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Zea mays
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KEYWORDS
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                                                                                                                                                                                             Bharti, AK and Messing, J: The Plant Gehome Initiative at Rutgers, Waksman Institute, Rutgers, The State University of New Jersey, 190 Frelinghuysen Road, Piscataway, NJ 08854, USA (http://pgir.rutgers.ed.)
Butler, E and Wing, R: Arizona Genomics Institute, Biological Sciences West, 448A, P.O. Box 210088, University of Arizona, Tucson, AZ 85721, USA (http://www.genome.arizona.edu)
Center project Information
Center project name: 130238
Center clone name: 309_E_13
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On Jan 14, 2005 this sequence version replaced gi:49035040. All repeats were identified using RepeatMasker: Smir, A.F.A. & Green, P. (1996-1997) http://ftp.genom.http://ftp.genom.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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/clone="zwmBBD0309E13"
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2923. 3022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2: contig of 2922 bp in length
2: gap of unknown length
7: gap of 12795 bp in length
7: gap of unknown length
8: contig of 9301 bp in length
8: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gap of unknown length
contig of 17224 bp in length
gap of unknown length
contig of 3352 bp in length
gap of unknown length
contig of 25522 bp in length
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unknown length
of 781 bp in length.
                                                                                                 Center: Broad Institute of MIT and Harvard Center code: WIBW Web site: http://www-seq.wi.mit.edu Contact: sequence_submissions@broad.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 36; DB 14; Pred. No. 1.9e-09;
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/organism="Zea mays"
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32782 CCCCCTAGACACACTCTAAGACACAACTTAAGACAC 32747 CCCCCTAGACACACTCTAAGACACAACTTAAGACAC 242

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/trānslation="wagtchyveflraopawalalaavgllvavraaarfalwyyaaf
Prokpelrrrygawavytgatdgigravafrlaasglglvlygrnoeklaavaabika
RH"
AF348367 1257 bp DNA linear PLN 02-MAR-2002
Zea mays inbred B77 beta-keto acyl reductase gene, partial cds.
AF348367
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                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 1257)

Dietrich,C.R., Cui,F., Packila,M.L., Li,J., Ashlock,D.A.,
Nikolau,B.J. and Schnable,P.S.

Nikolau,B.J. and Schnable,P.S.

Maize Mu transposons are targeted to the 5' untranslated region of the gl8 gene and sequences flanking Mu target-site duplications exhibit nonrandom nucleotide composition throughout the genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and Genetics, Iowa State
Ames, IA 50011, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1257;
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/product="beta-keto acyl reductase"
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100.0%; Pred. No. 6.1e-09;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="beta-keto acyl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (12-FBB-2001) Zoology
University, B420 Agronomy Hall,
Location/Qualifiers
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Best Local Similarity 100.
Matches 35; Conservative
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